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اعلمه باع تمنون بأماهوه بأماده باعداده الماده الماد	May 18, 2004, 16:14	. US-10-681-972-12 score: 286 : 1 gggaattcggatccaagaaa	table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	d: 3470272 seqs, 21671516995 residues	number of hits satisfying chosen parameters: 6940544	n DB seq length: 0 n DB seq length: 200000000	cocessing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries	GenEmbl:* 1
راماند WO		Title: Perfect score: Sequence:	table	Searched:	Total number o		Post-processing	Database :

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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175	61.2	288		139553	A39553 Sequence 41
175	61.2	288		IR130280	AR130280 Sequence
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1,2.2	59.8	243		1X412406	AX412406 Sequence
171	59.8	243		X412601	AX412601 Sequence
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20.72	fince 12 689 689.1	from patent GI:3972143	om pater:	us 5773696.	
SOURCE Unknown ORGANISM Unknown Unclass	Unknown. Unknown. Unclassified.				
REFERENCE 1 (bases AUTHORS Liang, J., TITLE Antifungal	ases 1 7,J., St ungal p	1 to 286) Shah, D. Maganlal. 1 polypeptide and	s) Kagar otide	, Wu,Y.Shun. methods for	and Rosenberger,C.Annette. controlling plant pathogenic
rungi JOURNAL Paten	t: US	5773696	. A-3	12 30-JUN-1998;	

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Unclassified.
1 (Dases 1 to 270)
Liang, J., Shah, D.Maganlal., Wu.Y.Shun. and Rosenberger, C.Annette.
Antifungal polypeptide and methods for controlling plant pathogenic
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94.1%; Score 269.2; DB 6; Length 270;
Best Local Similarity 99.3%; Pred. No. 1.3e-66;
Matches 268; Conservative 2; Mismatches 0; Indels 0.
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/organism="unknown"
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1 (bases 1 to 286)
Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
Antifungal polypeptide AlyAFP from Alyssum and methods for
controlling plant pathogenic fungi
Patent: US 6653280-A 12 25-NOV-2003;
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Matches 286; Conservative 0; Mismatches 0;
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ACCESSION AR432386 VEYWORDS SOURCE ORGANISM Unknown. ORGANISM Unknown. ORGANISM Unklown. ORGANISM Unklown. ORGANISM Unklown. AUTHORS AUTHORS ALIGHUNGAID DAYARPE from Alyssum and methods for controlling plant pathogenic fung; JOURNAL PATHORS Location/Qualifiers SOURCE /organism="unknown" /mol_type="genomic DNA"	Query Match 75.7%; Score 216.6; DB 6; Length 500; Best Local Similarity 91.6%; Pred. No. 1.8e-51; Matches 241; Conservative 0; Mismatches 19; Indels 3; Gaps 1; Qy 11 ATCCAAGAAAGTAATAGGCTAAGTTGCTACCATCATCTTTTTTTT	QY 71 TCTTGTTCTTTGCTGCTCTTTGAAGCACCAACAATGGTGGATGCAAGGTTGTGCGA 127 Db 110 TCTTGTTCTTTTGCTGCTTTTGAAGCACCAGCAATGGTGGAGTCACGGAAGTTTGTGCGA L28 GAGACCAAGTGGTCAGGAGTTTGTGGGAACAATGCATGCA	230 CAGAAACCTIGAAAGAGAGAACACGGATCTIGCAACTATGTTCCCAGCTCACAATG 248 TATTIGTTACTTCCCAIGTTAAT 270 290 TATTIGTTACTTCCCAIGTTAAT 312	AR014682 AR014682 LOCUS LOCUS LOCUS DEFINITION Sequence 5 from patent US 5773696. ACCESSION AR014682.1 GI:3972136 KEYWORDS SOURCE UNKNOWN. ORGANISM UNKNOWN.	REFERENCE 1 (bases 1 to 308) AUTHORS Liang,J., Shah,D.Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette. TITLE Antifungal polypeptide and methods for controlling plant pathogenic JOURNAL Patent: US 5773696-A 5 30-JUN-1998; FEATURES Location/Qualifiers SOURCE 1.308 Appropriate Patent 1.308	ORIGIN Query Match Query Match Best Local Similarity 86.1%; Score 190.8; DB 6; Length 308; Best Local Similarity 86.1%; Pred. No. 4.9e-44; Matches 223; Conservative 0; Mismatches 33; Indels 3; Gaps 1; Qy 11 AȚÇCAAGAAAGTAAȚAGATATGGCTAAGTTTGCTACCTTCTTTTGCTGC 70	DD 50 ATCACAGAAGTAATAGATATGGCTAAGTGTGCTTCCATCATCTCTCTTGTTGCTGCTGC 109 Qy 71 TCTTGTTCTTTGCTGCCTTTGAAGCACCAACAACGATGGATG
Matches 268; Conservative 2; Mismatches 0; Indels 0; Gaps 0; QY 9 GGATCCAAGAAAGTAAAGATATGGTAAGTTTGCTACCATCATCTTCTTTTGCT 69 Db 1 GGATCCAAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	Db 181 AGAAACCTTGAAAGAGCAGAACTGCAACTATGTCTTCCCAGCTCAAATGT 240 Qy 249 AITTGTTACTTCCCATGTTAATAAGGATCC 278 Db 241 ATTTGTTACTTCCCATGTTAATAAGGATCC 270 RESULT 5	_ =	AUTHORS Liang, J., Shah, D. Maganlal., Wu, Y. Shun. and Rosenberger, C. Annette. TITLE Antitungal polypeptide and methods for controlling plant pathogenic fungi most processed by 100 Tent. US 5773696-A 9 30-JUN-1998; Jooration/Qualifiers source /organism="uuknown" / mol_type="unassigned DNA"	Ouery Match Query Match Query Match Best Local Similarity 91.6%; Pred. No. 1.8e-51; Matches 241; Conservative 0; Mismatches 19; Indels 3; Gaps 1; Qy	11 TCTTGTTCTCTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCAAGGTTGTGCGA	QY 188 CAGAAACCTEGAAGAGGAACAGGGATCTTGCAACTATGTCTTCCAGCTCACAAATG 247 Db 230 CAGAAACTTGAAAGAGCAGAACCTTGCAACTATGTCTTCCCAGCTCACAATG 289 QY 248 TATTTGTTACTTCCCATGTTAAT 270 Db 290 TATTTGTTACTTCCCATGTTAAT 312	RESULT 6 AR432386 LOCUS AR432386 DEFINITION Sequence 9 from patent US 6653280.

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26. .265
/codon_start=1
/product=antifungal_protein"
/protein_id="AB03224.1"
/db_xref="G1:1399230"
/translation="WAKFASIITLLFAALVVFAAFBAPTMVBAKLCERSSGTWSGVCGNNANACKNQCIRLEGAQHGSCNYVFFAHKCICYFPC"
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales, Brassicaceae, Raphanus.
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/note="transcript putatively induced by Screrotinia
screrotium in infected Brassica napus"
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                                                                                      Sohn, U., Lee, C.M., Lee, M.H. and Kim, J.H.
Direct Submission
Submitted (129-MAY-1996) Department of Genetic Engineering,
Synogpook National University, Puk-Ku, Sankyuk-Dong 1370,
702-701, Korea
On Jul 1, 1996 this sequence version replaced gi:1293377.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Terras, F.R.G., Goderis, I.J., Penninckx, I.J., Osborn, R.W.
Broekaert, W.F.
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 8; Length 451;
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Direct Submission
Submitted (09-APR-1996) F.R.G. Terras, Institut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.2%; Score 186.6; DB 8;
larity 85.9%; Pred. No. 7.8e-43;
Conservative 0; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             475 bp mRNA R. Sativus mRNA for antifungal protein 3. X97319
 1 (bases 1 to 451)
Sohn, U., Lee, C.M., Lee, M.H. and Kim, J.H.
Brassica napus cDNAs
                                                                                                                                                                                                                                             /organism="Brassica napus"
                                                                                                                                                                                                                                                            /mol_type="mRNA"
/cultivar="Naehan"
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AFP; antifungal protein 3.
Raphanus sativus (radish)
Raphanus sativus
                                                                            (bases 1 to 451)
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                                                                                                                                                                                                                        . .451
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207; Conserv
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Best Local S
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RSEFP3
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Brassica napus
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                  CATTAACCTTGAAGGAGCNCGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 TCTTGTTCTTTTGCTGCTTTTTGAAGCACCAGCAATGGTGGAGTCACGGAAGTTGTGTGCGA 169
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                                                                      GAGTCCAAGTGGAACATGGTCAGGCGTGTGTGGAAACAACAATGCTTGCAAGAATCAGTG 229
                                                                                                           188 CAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGGTCACAAATG 247
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110 TCTTGTTCTTTTGCTGCTTTTGAAGCACCAGCAATGGTGGAGTTCACGGAAGTTGTGCGA 169
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                                    11 ATCCAAGAAAGTAATAGATATGGCTAAGTTTGCTACCATCATCTTCTTTTTTGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Unclassified.

1 (bases 1 to 308)

1 idang, J., Shah, D.M., Wu, Y.S. and Rosenberger, C.A.

Iniang, J., Shah, D.M., Wu, Y.S. and Rosenberger, C.A.

Antifungal polypeptide AlyARP from Alyssum and methods for controlling plant pathogenic fungi

Patent: US 6653280-A 5 25-NOV-2003;

Location/Qualifiers
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US9459 H07366
U59459.1 GI:1399229
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Best Local Similarity 86.1%; Pred. No. 4.9e-44;
Matches 223; Conservative 0; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                  DNA
                                                                                                                                                                                                                                                                                                        308 bp
Sequence 5 from patent US 6653280.
AR432382.1 GI:40194659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .308
/organism="unknown"
                                                                                                                                                                                   248 TATTTGTTACTTCCCATGT 266
                                                                                                                                                                                                        CATALGCTACTTCCCCTGT 308
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BNU59459
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DEFINITION
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AR432382
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DEFINITION
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AB012871
Wasabia japonica mRNA for gamma-thionin1, complete cds.
AB012871
AB012871. GI:11691893
gamma-thionin1.
Butrema wasabi
Eutrema wasabi
                                                                                    MASAHIRO NISHIBARA,SABURO YAMAMURA
CIZNIS/09,A01HS/00,A01N63/00,C07K14/415,C12N5/10,C12P21/02//
(C12N15/09,C12R1:91),(C12N5/10,C12R1:91),(C12P21/02,C12R1:91),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales, Brassicaceae, Eutrema.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTGAAGCACCATCAATGGTGGAAGCGCAGAAGTTGTGCGGAAAGTCAAGTGGGACATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 ICAGGAGITIGIGGGAACAACAAIGCAIGCAGGAACCAAIGCAGAAACCITGAAAGAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
PD 16-NOV-1999
PF 30-APR-1998 JP 1998121303
PR MASAHIRO NISHIBARA, SABURO YAWAMURA
PC C12N15/09, A01145/00, A01N63/00, C07K14/415, C12N5/10, C12PPC C12N15/09, C12R1:91), (C12N5/00, C12R1:91), (C12N5/00, C12R1:91), C12N5/00, C12R1:91) CC C12N5/00, C12R1:91), (C12N5/00, C12R1:91) CC C12N5/00, C12R1:91), CTR1:91, CTR1:91, CTR1:91, CTR2 C12N5/00, C12R1:91), CTR2 C12N5/00, C12R1:91, CC C12N5/00, C12R1:91, CTR2 C12N5/00, C1
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Saitch, H., Kiba, A., Nishihara, M., Yamamura, S., Suzuki, K.
Terauchi, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 414;
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21071227
11204773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 62.9%; Score 179.8; DB 6; Best Local Similarity 84.3%; Pred. No. 7.2e-41; Matches 215; Conservative 0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                           1. .414
/organism="Eutrema wasabi"
/mol_type="genomic DNA"
/db_xref="taxon:75806"
                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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Nishihara,M. and Yamamura,S.
Direct Submission
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| db_xref="SWISS-PROT:024332"
| translation="WAKFASIVALLFAALVVFAAFEAPTVVEAKLCERSSGTWSGVCG
NNNACKNQCIRLEGAQHGSCNYVFPAHKCICYFPC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 ITCTCTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCAAGGTTGTGCGAGAGACCAA 135
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Eutrema wasabi
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Eutrema.

1 (bases 1 to 414)
Masahiro, N. and Saburo, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73
     und Entwicklungsbiologie, Weinberg 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAAATGTATTTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 AGAAAGTAATAGATATGGCTAAGTTTGCTACCATCATCTCTTCTTCTTTTGCTGCTCTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 ATACATCAAAAATCATGGCTAAGTTTTGCTTCTATCGTCGCCCTTCTTTTCGCTGCTCTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 GTGGAACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 Tridahaddacacaacardarddarcrrrgcaacrargrarrcccrgcrcacaagrgrarcrgcr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                      /db_xref="taxon.3726"
/dev_stage="adult plants infected with Alternaria
brassicola"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 475;
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                                                                                                                                         /mol_type="mRNA"
/cultivar="Ronde Rode Kleine Witpunt"
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Antibacterial protein gene of horseradish.
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Pred. No. 1e-42;
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Patent: JP 1999313678-A 1 16-NOV-1999;
WATE PRES japonica
OS Wasabia japonica
PN JP 1999313678-A/1
                                                                                                                                                                                                                                                                                                                                                                                  Codon_start=1
Product="antifungal protein 3"
(protein id="CAA6598.1"
(db_xref="GI:1655685"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="AFP"
/product="antifungal protein 3"
                                                                                                             organism="Raphanus sativus"
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Pflanzenbiochemie, Stress- ur
Halle (Saale), D-06120, FRG
Location/Qualifiers
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JP 1999313678-A/1
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E31545.1 GI:13017385
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83.1%;
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                                                                                                                                                                                                                                                                                                 'gene="AFP"
28. .267
                                                                                                                                                                                                                                                                                                                                                   gene="AFP"
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Eutrema wasabi
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                                                                                      . .475
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Best Local S:
Matches 212
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VERSION
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E31545
LOCUS
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SOURCE
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/evidence-experimental
/product="antifungal protein 1 preprotein"
/protein id="AAA69541.1"
/db_xref="fd1:603122"
/translation="WAKFASIIALIPAALVLFAAFEAPTMVEAQKLCERPSGTWSGVC
                                                                                                                                                                                                                                                                                                                                                                                /function="antifungal, fungistatic" /note="Evidence for antifungal activity: Analysis of two novel classes of antifungal proteins from radish (Raphanus sativus L.) seeds. Terras, F.R.G. et al. (1992), J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGAGAGACCAAG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124
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1 (Dases 1 to 414)

Brockaert, W.F., Cammue, B.P.A., Terras, F.R.G., Vanderleyden, J., Brockaert, W. and Rees, S.B.

BIOCIDAL PROFEINS

Patent: WO 9305153-A 33 18-MAR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 TTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 AGTAATAGATATGGCTAAGTTTGCTACCATCATCTCTCTTCTCTTTTGCTGCTCTTGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 ATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTTGCTGCTCTTCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAAATGTATTTGTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 8; Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cch 62.5%; Score 178.8; DB 8; Length al Similarity 84.3%; Pred. No. 1.4e-40; 214; Conservative 0; Mismatches 37; Indels
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                                                                                                                        function="antifungal, fungistatic"
                                                                                                                                                                                                                                                                                                                                                                 product="antifungal protein 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="18 A nucleotides"
                                                                                                                                                                                                                                                                                                                                                                                                                                              sativus L.) seeds. Ter.
Chem. 267, 15301-15309"
/citation=[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=experimental
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            db xref="taxon:3726"
                               'tissue_type="seed"
1. .395
'gene="Rs-AFP1"
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                                                                                                                                                                                                                                                                                                         gene="Rs-AFP1"
                                                                                                                                                                                                                                                                                                                            102. .254
/gene="Rs-AFP1"
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                                                                                                           gene="Rs-AFP1"
                                                                                                                                                  codon_start=1
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A26875
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Best Local S:
Matches 214
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ACCESSION
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                                                   gene
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A26875
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KEYWORDS
SOURCE
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                                                                                               /codon_start=1
/codon_start=1
/product= gamma-thionin1"
/protein_id="BAB19054.1"
/db_xref="G1:11691894"
/translation="WAKFASIIALLFAALVLFSAFFAAPSMVEAQKLCEKSSGTWSGVC
GNNNACKNQCINLEGARHGSCNYIFPYHRCICYFPC"
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Raphanus Bativus antifungal protein 1 preprotein (Rs-AFP1) mRNA,
complete cds.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Raphanus.
I (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Terras, F.R.G., Eggermont, K., Kovaleva, V., Raikhel, N.V., Osborn, R.W., Kester, A., Rees, S.B., Torrekens, S., Van Leuven, F., Vanderleyden, J., Cammue, B.P.A. and Broekaert, W.F. Small cysteine-rich antifungal proteins from radish: their role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (14-DEC-1994) Franky R. Terras, F.A. Janssens Laboratory
of Genetics, Applied Biological Sciences, W. De Croylaan 42,
Heverlee, Belgium, B-3001
On Feb 9, 1995 this sequence version replaced gi:609321.
                                                                                                                                                                                                                                                                                                                                                                                                       83
                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                     30 ATGCTAAGTTTGCTACCATCATCTCTTCTTTTGCTGCTCTTTGTTCTCTTTGCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTGAAGCACCAACAATGGTGGATGC---AAGGTTGTGCGAGAGACCAAGTGGGACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 TTTGAAGCACCATCAATGGTGGAAGCGCAGAAGTTGTGCGAGAAGTCAAGTGGGACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 GAACACGGATCTTGCAACTATGTCTTCCCAGCTCAAATGTATTTGTTACTTCCCATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCAGGAGTTTGTGGGAACAACGATGCATGCAGGAACCAATGCAGAAACCTTGAAAGAGCA
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/organism="Eutrema wasabi"
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/db_xref="taxon:75806"
/tissue_type="leaf and stem"
1. .243
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2 (bases 1 to 395)
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88. .240
/product="unnamed"
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                                                                                                                                                                                                                                                                                        TGAAAGAGAGAACAGGATCTTGCAACTATGTCTTCCCAGCTCACAAATGTATTTGTTA 256
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unidentified
unclassified.
1 (bases 1 to 414)
Dubock, A.C., Powell, K.A. and Rees, S.B.
ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBICTIC MICROORGANISMS
PARENT: WO 9416076-A 37 21-JUL-1994;
ZENECA LTD (GB)
Other publication AU 5820494 940815.
                                                                                                                                            3;
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                                                                                                               cch 62.5%; Score 178.8; DB 6; Length 11 Similarity 84.3%; Pred. No. 1.4e-40; 214; Conservative 0; Mismatches 37; Indels
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Pred. No. 1.4e-40;
0; Mismatches 37;
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                         1. 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A39549 414 bp
Sequence 37 from Patent W09416076.
A39549. GI:2295842
            Location/Qualifiers
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Best Local Similarity 84.3%;
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Best Local S:
Matches 214
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Db 186 TGAGAAAGCACGACATGGAACTATGTCTTCCCAGGTCTAGGTA 245

Qy 257 CTTCCCATGTTAAT 270

Db 246 CTTCCTTGTTAAT 259

Search completed: May 18, 2004, 17:59:03

Job time: 1407.95 secs
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WO9737024-A2
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Aaz39124 Wasabia j
Abg82690 Wasabia j
Aav10632 A. thalia
Aav10633 A. thalia
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Rs-AFP1 c
Antimicro
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Rs-AFP2 c
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Aat94582 Amplified
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                                                  May 18, 2004, 16:12:26 ; Search time 278.85 Seconds (without alignments) 4357.126 Million cell updates/sec
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                                                                                                         1 gggaattcggatccaagaaa........taataaggatccgaattccc 286
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Aaq38650 F
Aaq70128 P
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Aat94581 (
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Aat68696 F
Aaz39124 V
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Aaq38652 B
Aaq70130 A
                                                                                                                                                                          6747726
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                      3373863 seqs, 2124099041 residues
                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                      Listing first 45 summaries
                                  OM nucleic - nucleic search, using sw model
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AAQ38650
AAQ70128
AAT72333
AAT68696
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ABQ82690
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AAV10633
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length
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Aag38651 Truncated	ß	N		ė.		44
Aaz99334 DNA encod	33	m	o,	36.6		43
Aaz99336 DNA encod	AAZ99336	m	Ω	۲.	107.4	42
Aaz99338 DNA encod	333	ო	æ		107.4	14
m	333	m	œ	ς.	107.4	40
Aaz99329 DNA encod	32	m	4	ζ.	107.4	39
Aaz99332 DNA encod	m	m	434	7.	107.4	38
99333 DNA	AAZ99333	'n	485		108.6	37
9337 DNA	AAZ99337	m	485	38.1	109	36
30 DNA	AAZ99330	m	443		110	32
Aaz99331 DNA encod	AAZ99331	٣	437	ъ.	111.6	34
Aat94580 Cloned 3'	AAT94580	N	306		111.6	33
DNA	ADC87758	σ	243		112.4	32
Aaz99325 DNA encod	AAZ99325	m	534		115.4	31
~	AAZ99327	m	534	ö	115.4	30
Aaz51396 Portion o	AAZ51396	m	534		115.4	59
Aaz99324 DNA encod	AAZ99324	ო	522	ö	115.4	28
Aaz99326 DNA encod	AAZ99326	m	909	ö	116.2	27
9	AAV10646	7	1616	42.2	20.	56
Aac46924 Arabidops	AAC46924	က	1973	•	155	25
Aaa53190 Raphanus	AAA53190	m	449	58.0	166	24

ALIGNMENTS

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This sequence encodes the mature protein of an antifungal polypeptide (AlyARP) isolated from plants of the genus Alyssum. The sequence was PCR amplified using primers AAT94583-194584, and the resultent 264 bp fragment was cloned as a BamHI fragment into the expression vector pMONZ3317 to generate plasmid pMONZ2552. The AlyARP sequence in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/product= "mature AlyAFP protein"
/note= "no start codon given at 5' end of sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alyssum antifungal polypeptide and corresponding DNA - used in the production of transgenic plants resistant to phytopathogenic fungi.
                                                                                                                                                                                                                                            Antifungal polypeptide; AlyAFP; inhibition; transgenic plant; phytopathogenic fungus; resistance; ss.
                                                                                                                                                                                  Alyssum species anti-fungal polypeptide AlyAFP cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosenberger CA;
                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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   BP.
AAT94574 standard; cDNA; 286
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P-PSDB; AAW35558.
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plasmid is placed under control of an B35S promoter and the maize HSP70 intron I sequence. The protein can be used to control phytopathogenic fungi, whilst the DNA can be used to produce transgenic plants that express the protein making them resistant to the phytopathogenic fungi
                                                                                                                                                                                                                                                                                                          TCTTTGCTGCTCTTGTTCTCTTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCAAGGT
                                                                                                                                                                                                                                   GGGAATTCGGATCCAAGAAGTAATAGATATGGCTAAGTTTGCTACCATCATCTCTTTC
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                                                                                                                                                               Gaps
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                                                                                                                            Length 286;
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                                                                                                                                                             Indels
                                                                                        Sequence 286 BP; 80 A; 62 C; 65 G; 79 T; 0 U; 0 Other;
                                                                                                                          100.0%; Score 286; DB 2;
100.0%; Pred. No. 4.8e-81;
ive 0; Mismatches 0;
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109. .258
                                                                                                                    Ouery Match
Best Local Similarity 100.º
Matches 286, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22. .108
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P-PSDB; AAW35560.
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                               This sequence represents the cDNA sequence cloned into the E. coli cassette vector pMON23317 to generate vector pMON22652. The cDNA encodes the antifungal polypeptide AlyAFP, isolated from plants of the genus Alyssum. The AlyAFP polypeptide can be used to control phytopathogenic fungi, whilst the coding DNA can be used to produce transgenic plants that express the polypeptide making them resistant to the phytopathogenic
                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                                                     AGAAACCTTGAAAGAGCAGAACACGGATCTTGCAAACTATGCCTTCGCAAATGT 248
                                                                                                                                                                                                                                                                                                                                                                     AGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAAATGT 240
                                                                                                                                                                                                                                                 GCTCTTGTTCTCTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCAAGGTTGTGCGAG 128
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                                                                                                                                                                                                    GGATCCAASAAAGTAATAGGTAAAGTTTGCTACCATCATCTCTTTTGCT
                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antifungal polypeptide, AlyAFP; inhibition; transgenic plant; phytopathogenic fungus; resistance; ss.
                                                                                                                                                   Score 269.2; DB 2; Length 270; Pred. No. 1.1e-75; 2; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "AlyAFP antifungal polypeptide"
                                                                                                                            Sequence 270 BP; 75 A; 58 C; 60 G; 75 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                          ATTTGTTACTTCCCATGTTAATAAGGATCC 270
                                                                                                                                                                                                                                                                                                                                                                                           ATTIGITACTICCCATGITAATAAGGATCC 278
                                                                                                                                                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alyssum species AlyAFP cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
           Example 4; Page 69; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВР
                                                                                                                                                   94.18;
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/*tag= a
/product=
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140. .289
/*tag= c
439. .443
/*tag= d
                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . .139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT99289 standard; DNA;
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                                                                                                                                                               Best_Local Simi
Matches 268;
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                                                                                                                                                    Query Match
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This sequence represents the cDNA sequence encoding the antifungal polypeptide AlyAFP, from plants of the genus Alyssum. The sequence represents a composite of the sequences isolated by 5' and 3' RACB (Rapid Amplification of CDNA Ends) methods (see AAT94577 and AAT94580). The AlyAFP polypeptide can be used to control phytopathogenic fungi, whilst the coding DNA can be used to produce transgenic plants that express the polypeptide making them resistant to the phytopathogenic fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 TCTTGTTCTCTTTGCTGCTTTTTGAAGCACCAGCAATGGTGGAGTCACGGAAGTTGTGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                  170 GAGTCCAAGTGGAACATGGTCAGGCGTGTGGGGAATAATAACGCATGCAGGAACCAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAAATGTCTTCCCCAGCTCACAAATG
                                                                                                                                                                                                                                                                                                              50 ATCACAGAAAGTAATAGATATGGCTAAGTGTGCTTCCATCATCTCCCTTGTCTCTGCTGC
                                                                                                                                                                                                                                                                                                                                           TCTTGTTCTCTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGA
                                                                                                                                                                                                                                                                                                                                                                                                      11 ATCCAAGAAAGTAATAGATATGGCTAAGTTTGCTACCATCATCTCTCTTTGCTGC
Alyssum antifungal polypeptide and corresponding DNA - used in the production of transgenic plants resistant to phytopathogenic fungi
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                                                                                                                                                                                                                        DB 2; Length 500;
                                                                                                                                                                                            Sequence 500 BP; 145 A; 89 C; 111 G; 154 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                       75.7%; Score 216.6; DB 2; llarity 91.6%; Pred. No. 9.2e-59; Conservative 0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cloned 5' region of antifungal polypeptide cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATTIGITACTICCCALGITAAT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rarricriacricccardinar 312
                                            Example 4; Page 67; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Page 65; 92pp; English.
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                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-MAR-1997;
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                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liang J,
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                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                          This sequence represents the cDNA sequence which encodes the antifungal polypeptide AlyAFP, isolated from plants of the genus Alyssum. The AlyAFP polypeptide can be used to control phytopathogenic fungi, whilst the coding DNA can be used to produce transgenic plants that express the polypeptide making them resistant to the phytopathogenic fungi
                                                                                                                                                                                                                                                                                                                                                                                                    130
                                                                                                                                                                                                                                                                                                                                                                                                                                  153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 AAACCTIGAAAGAGCAGAACACGGAICTIGCAACIAIGICTITCCCAGCICACAAAIGIAI 273
                                                                                                                                                                                                                                                                                                                                           70
                                                                                                                                                                                                                                                                                                                                                                       93
                                                                                                                                                                                                                                                                                                                                                            TCTTGTTCTCTTTGCTGCCTTTTGAAGCACCAATGGTGGATGCAAGGTTGTGCGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                     TCTTGTTCTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCAAGGTTGTGCGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAAATGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Composite cDNA sequence for Alyssum species antifungal polypeptide.
                                                                                   Alyssum antifungal polypeptide and corresponding DNA - used in the
                                                                                                    production of transgenic plants resistant to phytopathogenic fungi
                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antifungal polypeptide; AlyAFP; inhibition; transgenic plant; phytopathogenic fungus; resistance; ss.
                                                                                                                                                                                                                                                                     Score 256.8; DB 2; Dred. No. 1.38-71; Indels
                                                                                                                                                                                                                                                   Sequence 481 BP; 147 A; 88 C; 91 G; 154 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                         11 ATCCAAGAAAGTAATAGATATGGCTAAGTTTGCTACCATCATCTC
                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wu Y, Rosenberger CA;
             Rosenberger CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGITACTICCCAIGITAAT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274 TTGTTACTTCCCATGTTAAT 293
                                                                                                                                Example 4; Fig 1; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP
                                                                                                                                                                                                                                                                               89.8%;
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                                                                                                                                                                                                                                                                                                Best Local Similarity 99.2
Matches 258; Conservative
             Wu Y,
                                         WPI; 1997-503109/46.
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                                                                                                                                                                                                                                                                                              Similarity
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             Shah D,
                                                         P-PSDB; AAW35560
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                                                                                                                                                                                                                                                                                Query Match
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             Liang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
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This sequence is the product of the amplification of the 5' region of the antifungal polypeptide AlyAFP, isolated from plants of the genus Alyssum, by a 5' RACE (Rapid Amplification of cDNA Ends) using primers AAT94575-194576. The AlyAFP polypeptide can be used to control phytopathogenic fungi, whilst the coding DNA can be used to produce transgenic plants that express the polypeptide making them resistant to the phytopathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                           CATTAACCTTGAAGGAGGNCGACATGGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          An antibacterial protein gene of Wasabia japonica - useful as a food- or
                                                                                                                                                                                                                                                                                                              110 icingincrciringciecninicaagcaccagcaargeresacrcacgaagricieda
                                                                                                                                                                                                                                                                                                                                                                           170 GAGTCCAAGTGGAACATGGTCAGGCGTGTGGAAAACAACAATGCTTGCAAGAATCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                         CAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGGTCACAAATG
                                                                                                                                                                                                                                                    ATCCAAGAAAGTAATAGATATGGCTAAGTTTGCTACCATCATCTCTCTTTTGCTGC
                                                                                                                                                                                                                                                                                    TCTTGTTCTCTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGA
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wasabia japonica antibacterial protein encoding cDNA SEQ ID NO:1.
                                                                                                                                                                                             3.
                                                                                                                                                              Score 190.8; DB 2; Length 308;
Pred. No. 1.3e-50;
0; Mismatches 33; Indels 3;
                                                                                                                                  78 A; 71 C; 78 G; 79 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wasabia japonica; antibacterial; food additive; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .243
/*tag= a
/product= "antibacterial protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ39123 standard; cDNA to mRNA; 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 12-13; 16pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATTIGITACTICCCAIGT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                308
                                                                                                                                                              66.7%;
86.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATATGCTACTTCCCCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
(first entry)
                                                                                                                                                                                            223; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-057353/05.
                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IWAT-) IWATE KEN
                                                                                                                                  Sequence 308 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAY57564
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01-MAR-2000
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                                                                                                                                                            Query Match
Best Local S:
Matches 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAAATGTATTTGTTACTTCCCATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGACATGGGATCTTGCAACTATATCTTCCCATATCACAGATGTATCTGTTACTTCCCATGT
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                                                                                                                                                                                                                                                                                                                                                                                             90 TITGAAGCACCAACAATGGTGGATGC---AAGGTTGTGCGAGAGACCAAGTGGGACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTGAAGCACCATCAATGGTGGAAGCGCAGAAGTTGTGCGAGAAGTCAAGTGGGAACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCAGGAGTTTGTGGGAACAACAATGCATGCAGGAACCAATGCAGAAACCTTGAAAGAGCA
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria; fungicide; bacteriocide; antibiotic; antifungal; gram positive; plant disease resistance; low toxicity.
                              from
                     The present sequence encodes an antibacterial protein isolated frow Wasabia japonica. The antibacterial protein can be used as a food additive. (Updated on 15-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                            ٠.
ص
                                                                                                                                                                                        Length 414;
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                                                                                                                                                                                                                                      37; Indels
                                                                                                                                 Sequence 414 BP; 108 A; 79 C; 80 G; 147 T; 0 U; 0 Other
                                                                                                                                                                               Score 179.8; DB 3;
Pred. No. 4.8e-47;
0; Mismatches 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
16. .256
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92GB-00003038.
92GB-00013526.
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                                                                                                                                                                               Query Match
Best Local Similarity 84.3%;
Matches 215; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255
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(first entry)
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25-JUN-1992;
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Rees SB;
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               Powell KA,
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                                       WPI; 1994-249223/30.
                                                                                                                                                                                                                          correct PN field.)
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                                                     P-PSDB; AAR57325
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               Dubock AC,
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                                             primer AAQ38640 was used together with AAQ38641 to generate a probe for screening a Raphanus sativus seed cDNA library. This primer corresponds to amino acids 2 to 7 of Re-APP1 and has a sense orientation. The 144bp product was partially re-amplified using AAQ38642 and AAQ38641 to give a 123bp product, which was further reamplified with the same primers and ignoxiganin-11-dUTP instead of dTTP to give a digoxiganin labeled PCR product. This was used to screen a lambda ZAPII cDNA library by in situ plaque hybridisation. Positive plaques were purified and subjected to two additional screening rounds with the same probe. Inserts were excised in vivo into the pBluescript phagemid form with the aid of helper phage R408. Inserts from 22 positive clones were excised by BcoRI digestion and their size compared by agarose gel electrophoresis. Four clones had insert sizes of approx. 400bp the others between 250-300bp. The inserts of the 4 largest clones were then sequenced and found to differ only in the length of their 5, and 3, UTN's. The longest sequence is given here.
                                                                                                                                                                                                                                                                                                                                                                                                            80 CTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGAGAGACCAAG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                    125
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                                     This cDNA represents the sequence of Rs-AFP1 from Raphanus sativus. PCR
                                                                                                                                                                                                                                                                                                                                                                                                                               66 TITTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGCCAAG
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                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                   Score 178.8; DB 2; Length 414; Pred. No. 1e-46; 0; Mismatches 37; Indels 3,
                                                                                                                                                                                                                                                                            Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
            Example 21; Fig 35; 110pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                   62.5%;
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                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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14-FEB-1995
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                                                                                                                                                                                                                                                                                                                                                                                                              Plant-derived antimicrobial proteins are expressed in endosymbiotic Clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with recombinant Cxc are protected against fungal disease. A suitable antimicrobial protein is Rs-AFPI from R. sativus. The full-length CDNA sequence of Rs-AFPI is given in AAQ70128. (Updated on 25-MAR-2003 to
Antimicrobial protein producing endo-symbiotic microorganisms - is produced by combining nucleic acids encoding the protein with an endophyte, useful for protecting plant hosts from esp. fungal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 CTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGAGAGACCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 ATTAGTGATCATGGCTAAGTTTGCGTCCATCATCGCACTTCTTTTGCTGCTCTTGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 Triticiticida de la companda del companda del companda de la companda del companda del companda de la companda de la companda del com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126 TGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .87, aa:Glu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Raphanus sativus antifungal protein I (Rs-AFP1) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'product= "antifungal_protein_1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 62.5%; Score 178.8; Best Local Similarity 84.3%; Pred. No. 1e-40
Matches 214; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (pos:85.
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                                                                                                                                                                                                                                                                                     Disclosure; Page 31; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag= a
'transl_except=
.6..102
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Radish antifungal protein 1 (Rs-AFP1) cDNA

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Antifungal peptide derived from radish antifungal protein 2 - and related DNA, useful for producing plants with increased fungal resistance and as therapeutic or preservative agent.
                                                                         Puijk WC, Schaaper WMM,
, Samblanx GW, Fant F,
                     96WO-GB003068
                                    95GB-00025455
96GB-00006552
                                                                                                                                                            8; Fig 2; 65pp;
                                                                                                       WPI; 1997-332786/30.
P-PSDB; AAW19280.
                                                          (ZENE ) ZENECA LTD
                                                                         Meloen RH, Puij
Broekaert W, Sa
Van Gelder WMJ;
                                    13-DEC-1995;
28-MAR-1996;
                     12-DEC-1996;
       19-JUN-1997
                                                                                                                                                                                                                                                                             field.
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protein (Rs-AFPI). Analogues of the homologue protein, Rs-AFPI (AAM19281), have also been produced (see AAM19282-92, AAM19294-98, AAM19301-04, AAM1930-14, AAM1930-14, AAM1930-1-04, AAM This cDNA sequence encodes an Rhapanus sativus (radish) antifungal

Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;

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136
                                                                                                   125
                                                                                                                        196
                                                                                                                                            185
                                                                                                                                                                256
                                                                                                                                                                                186 TGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCAGCTCACAAGTGTATCTGCTA 245
                                         79
                                                            65
                                                                              CTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGAGAGACCAAG
                                                    66 TTTTGCTGCTTTCGAAGCACCACAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAG
                                                                                                                     TGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAAATGTATTTGTTA
                                      Gaps
                     3;
 Length 414;
                     Indels
                    37;
Score 178.8; DB 2;
Pred. No. 1e-46;
                   0; Mismatches
62.5%;
84.3%;
                                                                                                                                                                                                      CTICCCATGITAAT 270
                    Conservative
                                                                                                                                                                                                                         CTTTCCTTGTTAAT
         Similarity
        Local Simi.
hes 214;
                                                                              80
                                                                                                                                                                                                                         246
                                                                                                                                                              197
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 Query Match
                   Matches
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79 65 136 125

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This cDNA clone codes for the preprotein for radish antifungal protein 1 (Rs-AFP1) (AAW19617). Novel antifungal proteins are based on Rs-AFP1, Rs-AFP2 (see AAW19616), Rs-AFP3 and Rs-AFP4, especially those in which Gly9 is repaced by Arg, Val39 by Arg, Gly9 by Arg, Glu5 by Met and/or Gly16 by Met. Mutants (see AAW26371-90) of Rs-AFP2 are specifically claimed. The mutants show improved salt tolerant antifungal activity, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTTGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAAGGCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAAATGTATTTGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 CTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGAGAGACAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 AGTAATAGATATGGCTAAGTTTGCTACCATCATCTCTTCTTCTTTTGCTGCTCTTGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 Arragicarcardecraactricecracearcarcecraticaring concretions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       New active mutants of radish antifungal protein 2 - used to generate fungus-resistant plants or as therapeutic or preservative agents.
                          Rs-AFP1; radish antifungal protein 1; fungicide; salt tolerance;
preservative; transgenic plant; crop protection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 178.8; DB 2; Length 414;
Pred. No. 1e-46;
0; Mismatches 37; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
                                                                                                                            *tag= a
transl except= (pos:85. .87, aa:Glu)
6. .102
                                                                                                                                                                                                                                                                                                                                                                                  Rees SB;
                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 2; 39pp; English
                                                                                                                                                                                                                                                                                                                                                                                 De Samblanx GW,
                                                                                                                                                                                                                                                                                           96WO-GB003065
                                                                                                                                                                                                                                                                                                                        95GB-00025474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 62.5%;
Best Local Similarity 84.3%;
Matches 214; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTCCCATGTTAAT 270
                                                                                                                                                                       /*tag≈ b
103. .255
/*tag= c
                                                                                                                  . .258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       when expressed in plants
                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1997-332785/30.
                                                                                                                                                                                                                                                                                                                                                    (ZENE ) ZENECA LTD.
                                                                    Raphanus sativus.
                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAW19617
                                                                                                                                                                                                                                                                                                                                                                               Broekaert WF,
                                                                                                                                                                                                                                                                                           12-DEC-1996;
                                                                                                                                                                                                                                                                                                                       13-DEC-1995;
                                                                                                                                                                                                                                                              19-JUN-1997
                                                                                                                                                          sig_peptide
                                                                                                                                                                                      mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99
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RESULT 11 AAZ39124

CTTTCCTTGTTAAT

246

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11 11 11

English.

related

Van Amerongen A;

Sijtsma L, Van Ameron Borremans FAM, Rees SB

AAT68696 standard; cDNA; 414

AAT68696

BP

13-DEC-1997

(first entry)

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The present invention describes a disease-resistant plant in which a wasabi gamma-thionin gene is introduced. Also described is a method for the creation of the above disease-resistant plant by introducing a wasabi gamma-thionin gene to a plant. The present sequence encodes a Butrema wasabi (Wasabia japonica) gamma-thionin protein from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TITGAAGCACCATCAATGGTGGAAGCGCAGAAGTTGTGCGAGAAGTCAAGTGGGACATGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wasabia japonica; gamma-thionin; plant; disease-resistant plant; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 CGACATGGATCTTGCAACTATATCTTCCCATATCACAGATGTATCTGTTACTTCCCATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 AIGGCIAAGTITGCIACCATCATCICTTTCTTTTGCTGCTCTTTGTTCTTTTGCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGGCTAAGTTTGCTTCTATCATCGCTCTTCTTCTTCGCTGCTCTTGTTCTCTTTTCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 TITIGAAGCACCAACAATGGTGGATGC---AAGGTTGTGCGAGAGACCAAGTGGGACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCAGGAGTTTGTGGGAACAACAATGCATGCAGGAACCAATGCAGAAACCTTGAAAGAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 GAACACGGAICTIGCAACTAIGTCTICCCAGCTCACAAAIGTATTIGTTACTICCCAIGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A disease-resistant plant in which wasabi gamma-thionin gene is introduced, creation of the disease-resistant plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62.0%; Score 177.4; DB 6; Length 243; larity 86.0%; Pred. No. 2.2e-46; Conservative 0; Mismatches 31; Indels 3
                                                         Wasabia japonica gamma-thionin encoding cDNA SEQ ID NO:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 243 BP; 60 A; 54 C; 55 G; 74 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                       "gamma-thionin"
                                                                                                                                                                                                                                                                Location/Qualifiers
1. .243
/*tag= a
/product= "gamma-thic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 8; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-MAR-2001; 2001JP-00083526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAR-2001; 2001JP-00083526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV10632 standard; DNA; 403
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P-PSDB; ABP53725.
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Les 209; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                             JP2002272292-A
                                                                                                                                                                                                            wasabi
   02-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                            Eutrema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loca
Matches
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   田袋袋袋品
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes an antibacterial protein isolated from Wasabia japonica. The antibacterial protein can be used as a food or feed additive. (Updated on 15-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 CGACATGGATCTTGCAACTATATCTTCCCATATCACAGATGTATCTGTTACTTCCCATGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAAATGTATTTGTTACTTCCCATGT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCAGGAGTTTGTGGGAACAACAATGCATGCAGGAACCAATGCAGAAACCTTGAAAGAGCA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTGAAGCACCATCAATGGTGGAAGCGCAGAAGTTGTGTGCGAGAAGTCAAGTGGGACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTGAAGCACCAACAATGGTGGATGC---AAGGTTGTGCGAGAGACCAAGTGGGACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 AIGGCIAAGTIIGCIACCAICAICTCTICICITIIGCIGCICTIGIICICTIIGCIGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    An antibacterial protein gene of Wasabia japonica - useful as a food-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Areacra Arricharda reacretarica recipiente de la reconstruction de la re
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                      Wasabia japonica antibacterial protein encoding cDNA SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 416 BP; 111 A; 77 C; 81 G; 147 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                             Wasabia japonica; antibacterial; food additive; ds.

    .243
/*tag= a
/product= "antibacterial protein"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 178.2; DB 3;
Pred. No. 1.6e-46;
0; Mismatches 38;
BP.
CDNA to mRNA; 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 13-14; 16pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABQ82690 standard; cDNA; 243 BP.
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Best Local Similarity 83.9%;
Matches 214; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAATTATTCTACCAA 255
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                                                                                                               (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-057353/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
   standard;
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                                                                                                            15-SEP-2003
01-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267
                                                      AAZ39124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147
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AAZ39124
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23-JUN-1998

RESULT 12
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                            Protecting plants against pathogens by inducing defensin genes - by stimulating ethylene or jasmonate pathways, also new promoter of defensin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGGGACATGGTCAGGAGTTTGTGGGAACAATGCATGCAGGAACCAATGCAGAAACC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence encodes the Arabidopsis PDF1.1 gene which is used in a novel method for the protection of plants against pathogens which involves inducing expression of a plant defensin gene by stimulating the jasmonate and/or ethylene pathways. The method is used to induce protection against necrotrophic pathogens, specifically fungi and does not require cytotoxic or potentially harmful chemicals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74
                                                                                                                                                                                                                                                                                                                                        Manners JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 AAACAATAGTCATGGCTAAGTCTGCTACCATCGTTACTCTTTTTCTTCGCTGCTCTTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTTTGCTGCCTTTGAAGCACCACAACAATGGTGGATGCA---AGGTTGTGCGAGAGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 TCTTTGCTGCTCTTGAAGCACCGATGCTGGAAGCACAGAAGTTGTGCGAGAGCCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 Grigdakarigercegagirirgegaaakcagraacegergeaagaareagiedarraace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCCAGCTCACAAATGTATTTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                        Defensin; PDF1.1; protection; plant; pathogen; jasmonate; ethylene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 403;
                                                                                                                                                                                                                                                                                                                                        Terras FRG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 403 BP; 112 A; 77 C; 85 G; 129 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.7%; Score 176.6; DB 2;
83.5%; Pred. No. 5e-46;
iive 0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                      Penninckx IAMA,
                                                                                                                                                                                     /note= "plant defensin"
                                                                                    Location/Qualifiers
26. .268
                                                                                                                                   /*tag= b
114. .265
/*tag= c
/product= "PDF1.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, Fig 1; 72pp; English
                                                                                                                                                                                                                                                              97WO-GB001672
                                                                                                                                                                                                                                                                                    96GB-00013753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTICCCAIGITAAT 269
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                                                                                                                                                                                                                                                                                                                                      Thomma BPHJ,
                                                                                                           /*tag= a
26. .113
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 83.5
Matches 213; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     gene from Arabidopsis.
                                                              thaliana.
                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-086663/08.
A. thaliana PDF1.1
                                                                                                                                                                                                                                                                                                             (ZENE ) ZENECA LTD
                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAW40345.
                                                                                                                                                                                                                                                                                                                                      Broekaert WF,
                                                                                                                                                                                                            WO9800023-A2
                                                                                                                                                                                                                                                             20-JUN-1997;
                                                                                                                                                                                                                                                                                    01-JUL-1996;
                                                            Arabidopsis
                                                                                                                         sig_peptide
                                                                                                                                                  mat peptide
                                     fungi; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       256
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Protecting plants against pathogens by inducing defensin genes - by stimulating ethylene or jasmonate pathways, also new promoter of defensin gene from Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 CTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGAGAGACCAAG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   novel method for the protection of plants against pathogens which involves inducing expression of a plant defensin gene by stimulating the jasmonate and/or ethylene pathways. The method is used to induce protection against necrotrophic pathogens, specifically fungi and does not require cytotoxic or potentially harmful chemicals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Manners JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 AATAATCATCATGGCTAAGTTTGCTTCCATCATCACCTTATCTTCGCTGCTTCTTGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence encodes the Arabidopsis PDF1.2 gene which is used in a
                                                                                                                                                                             Defensin; PDF1.2; protection; plant; pathogen; jasmonate; ethylene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.6%; Score 176.2; DB 2; Length 400; 83.8%; Pred. No. 6.7e-46; ive 0; Mismatches 38; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Penninckx IAMA, Terras FRG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 400 BP; 109 A; 82 C; 80 G; 125 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= c
/product= "PDF1.2"
/note= "plant defensin"
                                                                                                                                                                                                                                                                                           Location/Qualifiers
32. .274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 1; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96GB-00013753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thomma BPHJ,
AAV10633 standard; DNA; 400
                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                            32. 119
/*tag= b
120. 271
                                                                                                                                                                                                                                                                                                                                       /*tag= a
32. .119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 83.8
Matches 212; Conservative
                                                                                                                                                                                                                                            Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-086663/08.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAW40346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Broekaert WF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9800023-A2
                                                                                                                                A. thaliana
                                                                                      23-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JAN-1998
                                                                                                                                                                                                                                                                                                                                                          sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
                                                                                                                                                                                                       fungi; ss
                                          AAV10633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137
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181 CGACATGGATCTTGCAACTATATCTTCCCATATCACAGATGTATCTGTTACTTCCCATGT 240
                                                                                                              Search completed: May 18, 2004, 17:22:39 Job time: 280.85 secs
                                             TAA 269
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                                             267
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TGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAAAGGTATTTGTTA 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a disease-resistant plant in which a wasabi gamma-thionin gene is introduced. Also described is a method for the creation of the above disease-resistant plant by introducing a wasabi gamma-thionin gene to a plant. The present sequence encodes a Eutrema wasabi (Wasabia japonica) gamma-thionin protein from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 TCAGGAGTTTGTGGGAACAACAATGCATGCAGGAACCAATGCAGAAACCTTGAAAGAGCA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207 GAACACGGAICTIGCAACTAIGTCTICCCAGCICACAAAIGIAITIGITACTICCCAIGT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09
                                                                                                                                                                                                                                                         Wasabia japonica; gamma-thionin; plant; disease-resistant plant; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Arggeraagringerietarearegeretereriegereteretereteretere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 AIGGCIAAGITIGCIACCAICATCICITITCITITIGCIGCICTIGITCICTITIGCIGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 TITGAAGCACCAACAATGGTGGATGC---AAGGTTGTGCGAGAGACCAAGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A disease-resistant plant in which wasabi gamma-thionin gene is introduced, creation of the disease-resistant plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 175.8; DB 6; Length 243; Pred. No. 7.2e-46; 0; Mismatches 32; Indels 3.
                                                                                                                                                                                                                               Wasabia japonica gamma-thionin encoding cDNA SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 243 BP; 59 A; 55 C; 55 G; 74 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .243
/*tag= a
/product= "gamma-thionin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 8-9; 11pp; Japanese.
                                                                                                                                                   BP.
                                                                                                                                                 ABQ82691 standard; cDNA; 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-MAR-2001; 2001JP-00083526.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.5%;
85.6%;
                                                    CTTCCCATGTTAA 269
                                                                      262 CGTCCCATGTTAA 274
                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 85.6
Matches 208; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-718704/78.
P-PSDB; ABP53726.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IWAT-) IWATE KEN
                                                                                                                                                                                                                                                                                                  Eutrema wasabi.
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                                                                                                                                                                                                      02-JAN-2003
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 197
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'Cgn2_G/ptodata2/ina/5A_COMB.seq:*
'Cgn2_G/ptodata2/ina/5B_COMB.seq:*
'Cgn2_G/ptodata2/ina/6A_COMB.seq:*
'Cgn2_G/ptodata2/ina/6B_COMB.seq:*
'Cgn2_G/ptodata2/ina/PCTUS_COMB.seq:*
'Cgn2_G/ptodata/2/ina/PCTUS_COMB.seq:*
'Cgn2_G/ptodata/2/ina/PCTUS_COMB.seq:*
                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-103-489-5

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US-08-177-192-48

US-08-777-192-48

US-08-777-192-48

US-08-777-192-88

US-08-777-192-58

US-08-977-981-16

US-08-977-981-16

US-08-977-982-58

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US-08-627-706-17

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US-09-133-181-17
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score: 286
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Patent No. 5773696
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: No. Yomie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES. 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 5773696th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
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100.0%; Pred. No. 9.2e-84;
tive 0; Mismatches 0;
US-08-627-706-8
US-09-103-489-8
US-08-377-687-50
US-08-377-687-50
US-08-777-192-50
US-08-777-192-50
US-08-627-706-11
US-09-103-489-11
US-09-103-489-11
US-08-377-687-31
US-08-377-687-31
US-08-777-192-33
US-08-777-192-33
US-08-777-192-34
US-08-977-192-34
US-08-977-192-34
US-08-977-192-34
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CLASSIFICATION: 436
ATTORNEY AGRAT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34.565
REFERENCE/COCKET WNOBER: 38-21(10700) A
TELECHOMIUNICATION INFORMATION:
TELEPRAN: (314)537-6224
TELEPRAN: (314)537-6047
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.0
Matches 286; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
  ZIP: 63198
COMPUTER READABLE FORM:
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APPLICANT: Internation:
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Wan, Younie S.
APPLICANT: Wan, Younie S.
APPLICANT: Rosenberger: Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALVAFP from Alyssum and Methods for Control TITLE OF INVENTION: Plant Pathogenic Fungi
FILE REPERBRUCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: 09/103,489
FRICA APPLICATION NUMBER: 09/103,489
FRICA APPLICATION DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE PATENT PATENT OF NOS: 20
SOFTWARE PATENT OF NOS: 20
        61 TCTTTGCTGCTCTTGTTCTCTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCAAGGT 120
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// OTHER INFORMATION: Synthetic PCR reaction product

US-09-829-381D-12
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Query Match

Best Local Similarity 100.0%; Pred. No. 9.2e-84;

Matches 286; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
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LENGTH: 286
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1 GGGAATTCGGATCCAAGAAAGTAATAGATATGGCTAAGTTTGCTACCATCATCTCTTC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/09103489
Patent No. 6215048
GENERAL INFORMATION:
APPLICANT: Liang, Uihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
                                                                                                                                                                                                                                                                                                                        241 ACAAATGTATTGTTACTTCCCATGTTAATAAGGATCCGAATTCCC 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 286;
                                                                                                                                                                                                                                                                                              241 ACAAATGTATTTGTTACTTCCCATGTTAATAAGGATCCGAATTCCC 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 286; DB 3;
100.0%; Pred. No. 9.2e-84;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: INP PC compatible
COMPUTER: INP PC compatible
SOFWARE: Patentin Release #1.0, Ver
SOFWARE: Patentin Release #1.0, Ver
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-UTN-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTATION NUMBER: 34-565
REFERROCE/DOCKET NUMBER: 38-21 (1070
TELECOMMUNICATION INFORMATION:
TELEFHONE: (314) 537-6224
TELEFHONE: (314) 537-6224
TELEFHONE: (314) 537-6047
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 286; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA
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CITY: St. Louis
STATE: Missouri
COUNTRY: USA
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APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OP SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 5773696th
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                     COUNTRY: USAN
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
FILING DATE:
CLASSIFICATION: 436
ATTORNON NUMBER: 34,565
ATTORNON NUMBER: 38-21(10700)A
FREGESTRATION NUMBER: 38-21(10700)A
TELECOMMONICATION NUMBER: 38-21(10700)A
TELECHMONICATION NUMBER: 38-21(10700)A
TELEFRAX: (314)537-6224
TELEFRAX: (314)537-624
TELEFRAX: (314)537-624
TELEFRAX: (314)537-624
SEQUENCE CHARACTERISTICS:
FROGUENCE CHARACTERISTICS:
FENGTH: 270 base pairs
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STRANDEDNESS: single
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                                                                                                                                                                                                   COUNTRY:
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US-09-103-489-14

Sequence 14, Application US/09103489

Patent No. 6215048

APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: No. Yonnie S.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi

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Defence 14, Application US/09829381D
Patent No. 6653280
Patent Rosenberger, Cindy A.
PITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control TITLE OF INVENTION: Plant Pathogenic Fungi
PITLE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/09/829,381D
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/103,489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 270;
                     CORRESPONDENCE ADDRESS:
ADDRESSEB: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 6215048th
                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-JUN-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: COADM. CHARLES E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700) A
TELECOMMUNICATION INFORMATION:
MEDISCOMMUNICATION INFORMATION:
MEDISCOMMUNICATION INFORMATION:
MEDISCOMMUNICATION INFORMATION:
MEDISCOMMUNICATION INFORMATION:
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Query Match

Best Local Similarity 99.3%; Pred. No. 2.7e-78; Matches 268; Conservative 2; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 270 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                             ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                         CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-829-381D-14
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Length 500;

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170 GAGTCCAAGTGGAACATGGTCAGGCGTGTGTGGGAATAATAACGCATGCAGGAACCAATG 229
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                                                                                                                                                                                                                                                   11 ATCCAAGAAAGTAATAGATATGGGTAAGTTTGCTACCATCATCTCTTTTTGCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                             230 CAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAAATG
                                                                                                                                                                                                                                                                                                                                       71 ICTIGITCTTTGCTGCCTTTGAAGCACCAATGGTGGATGCA---AGGTTGTGCAA
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Fatent No. 6215048

GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 6215048th
STATHER: Missouri
                                                                                                                                                                75.7%; Score 216.6; DB 1; Length 91.6%; Pred. No. 5e-61; Live 0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE PACETIES FOLLOS/MS-DOS
SOFTWARE PACETIES FOLLOS/MS-DOS
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-JUN-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: COChen, Cherles E.
REGISTRATION NUMBER: 34.565
REFERENCE/DOCKET NUMBER: 34.565
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 537-624
TELECOMMUNICATION SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 TATTTGTTACTTCCCATGTTAAT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 TATTTGTTACTTCCCATGTTAAT 270
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                                                                                                                                                         Query Match
Best Local Similarity 91.69
Matches 241; Conservative
             500 base pairs
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TYPE: nucleic acid
STRANDEDNESS: single
                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                          ; TOPOLOGY: linear; MOLECULE TYPE: CDNAUS-08-627-706-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63198
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US-09-103-489-9
             LENGTH:
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                                                                                                                                                                                                                                        94.1%; Score 269.2; DB 4; Length 270; 99.3%; Pred. No. 2.7e-78; tive 2; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/08627706
Patent No. 5773696
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F STREET: 700 Chesterfield Village Parkway No. 5773696th CITY: St. Louis STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Cohen, Charles B.
REGISTRATION NUMBER: 34.565
REFERENCE/DOCKET NUMBER: 38-
TELECOMMUNICATION INFORMATION:
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 14
LENGTH: 270
                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
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TELEPAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                     ; FEATURE:
; OTHER INFORMATION: Plasmid
US-09-829-381D-14
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.3
Matches 268; Conservative
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CLASSIFICATION: 436
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                                                                                                                                                                                                                                                    APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 5773696th
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 66.7%; Score 190.8; DB 1; Best Local Similarity 86.1%; Pred. No. 1e-52; Matches 223; Conservative 0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38-21 (10700) A
                                                                248 TATITGITACTICCCAIGITAAT 270
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Patent No. 5773696
GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: COhen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21
TELECOMMUNICATION INFORMATION:
TELEPHORE: (314,537-624
TELEFAX: (314,537-624
TELEFAX: (314,537-604)
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248 TATITGITACTICCCAIGT 266
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nucleic acid
EDNESS: single
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CITY: St. Louis
STATE: Missouri
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APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Wosenberger, Clindy A.
TITLE OF INVENTION: Antitungal Polypeptide ALYAFP from Alyssum and Methods for Contro TITLE OF INVENTION: Plant Pathogenic Fungi
TITLE OF INVENTION: Plant Pathogenic Fungi
TITLE OF INVENTION: Plant Pathogenic Fungi
CURRENT APPLICATION NUMBER: US/09/829,381D
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR PILING DATE: 1998-06-24
NUMBER OF SEQ 1D NOS: 20
SOFTWARE: PatentIn version 3.1
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                                                      tch 75.7%; Score 216.6; DB 3; Length 500; al Similarity 91.6%; Pred. No. 5e-61; 241; Conservative 0; Mismatches 19; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.7%; Score 216.6; DB 4; Length 500; 91.6%; Pred. No. 5e-61; tive 0; Mismatches 19; Indels 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 9, Application US/09829381D
; Patent No. 6653280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 75.7
Best Local Similarity 91.6
Matches 241; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Alyssum spp
; MOLECULE TYPE:
US-09-103-489-9
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                                                        Query Match
Best Local S
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Indels
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Pred. No. 1e-52;
0; Mismatches 33;
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OTHER INFORMATION: Synthetic PCR reaction product
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Patent No. 5538252
GENERAL INFORMATION:
APPLICANT: BROBKABRT, WILLEM F.
APPLICANT: CAMMUE BRUNO P.A.
APPLICANT: CAMMUE BRUNO P.A.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEBE: CUSHWAN DARBY & CUSHWAN
STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: misc_feature
; LOCATION: (22)..(248)
; COTATION: N= any nucleotide
US-09-829-381D-5
                                              Sequence 5, Application US/09829381D Patent No. 6653280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 TATTIGITACTICCCAIGT 266
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Best Local Similarity 86.1%;
Matches 223; Conservative (
                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Seguence
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                                                                                    GENERAL INFORMATION:
                              US-09-829-381D-5
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LENGTH: 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 ATCCAAGAAAGTAATAGATATGGCTAAGTTTGCTACCATCATCTCTCTTTTTTTGCTGC
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                                                                                                         Sequence 5. Application US/09103489
Patent No. 6215048
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Nosenberger, Cindy A.
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
                                                                                                                                                                                                                                                                                                                               E: Charles E. Cohen, Monsanto Company, BB4F 700 Chesterfield Village Parkway No. 6215048th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-JUN-1998
CLASSIFICATION: 8000
CLASSIFICATION: 8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 190.8; DB 3;
Pred. No. 1e-52;
0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21
TELECOMMUNICATION INFORMATION:
TELEFAX: (314) 537-624
INFORMATION FOR SEQ ID NO: 5:
290 CATATGCTACTTCCCCTGT 308
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Best Local Similarity 86.1%;
Matches 223; Conservative
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LENGTH: 308 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                       STREET: 700 COLUMN STREET: 700 COLUMN STATE: Missouri STATE: Wissouri USA
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APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger. Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control
TITLE OF INVENTION: Plant Pathogenic Fungi
TITLE OF INVENTION: Plant Pathogenic Fungi
CURRENT APPLICATION NUMBER: 1909/829,381D
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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80 CTITGCTGCCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGAGAGACCAAG 136
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CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 16,773
REJECOMMUNICATION INFORMATION:
TELEPOME: 202-861-3000
TELEPAX: 202-82-0944
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs
TYPE: nucleic acid
STRANDENNESS: both
                                                                                                                                    ZIP: 20005
COMPUTER READABLE FORM:
MADIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/777,192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.5%; Score 178.8; DB 1;
84.3%; Pred. No. 9.7e-49;
Live 0; Mismatches 37;
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OSBORN, RUPERT W.
REES, SARAH B.
TERRAS, FRANKY R.G.
VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 48, Application US/08971982
Patent No. 6187904
GENERAL INFORMATION:
APPLICANT: BROEKAERT, WILLEM F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257 CTTCCCATGTTAAT 270
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Matches 214; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: CDNA
                                   WASHINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
US-08-777-192-48
                                   CITY: WA
STATE: D
COUNTRY:
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US-08-971-982-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 800
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELEBHONE: 202-861-3000
TELEBHONE: 202-861-3000
TELEBHONE: 202-862-0944
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 48, Application US/08777192
Patent No. 5824669
GENERAL INFORMATION:
APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: OSBOOKN, RUPERT W.
APPLICANT: OSBOOKN, RUPERT W.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: TERRAS, ERANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CUSHMAN DARBY & CUSHMAN
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Matches 214; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: 16..255
US-08-377-687-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: CDNA
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US-08-777-192-48
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80 CITTGCTGCCTITGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGAGAGACCAAG 136
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NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSE: CUSHMAN DARBY & CUSHMAN
CITY: WASHINGTON
CITY: WASHINGTON
CITY: WASHINGTON
COMPITER READABLE FORM:
MEDITOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PATCATION DATA:
COMPUTER APPLICATION NUMBER: US/08/971,982
FILING DATE: 17-NO. 6187904-1997
CLASSIFICATION NUMBER: US/08/971,982
FILING DATE: 17-NO. 6187904-1997
CLASSIFICATION NUMBER: US/08/002,480
FILING DATE: OLJAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
RECISTRATION NUMBER: 16,773
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TELEFAX: 202-861-3000
TELEFAX: 202-862-0944
INFORMATION PRO SEQ ID NO: 48
STRANDENCES: DOLD
TELEFAX: 202-861-3000
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; LOCATION: 16..255
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-08-971-982-48
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MOLECULE TYPE: cDNA
FEATURE:
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Search completed: May 18, 2004, 19:02:18 Job time : 59.5 secs

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Sequence 14, Appl
Sequence 14, Appl
Sequence 9, Appli
Sequence 9, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 48, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 15, Appl
Sequence 15, Appl
                                              May 18, 2004, 17:59:12 ; Search time 263.25 Seconds (without alignments) 4930.226 Million cell updates/sec
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                                                                                                                                                                                                                                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-006-252A-19
US-09-732-561-13
US-09-732-561-15
US-09-887-576-607
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US-09-82-381A-14

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US-09-823-381A-9

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                                                                                                                                           2947324 seqs, 2269024515 residues
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                               OM nucleic - nucleic search, using sw model
                                                                                                                 IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Match Length
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15 175 61.2 288 9 US-09-759-584-58 Sequence 58, Appl 174.2 60.9 243 9 US-09-938-842A-2046 Sequence 2046, Ap 18 172.2 60.2 285 11 US-09-938-842A-2046 Sequence 16, Appl 19 US-09-829-381A-16 Sequence 16, Appl 20 US-09-829-381A-16 Sequence 16, Appl 20 US-09-829-381A-17 Sequence 17, Appl 20 US-09-732-561-21 Sequence 17, Appl 20 US-09-732-561-21 Sequence 17, Appl 20 US-09-732-561-21 Sequence 21, Appl 20 US-09-732-561-21 Sequence 21, Appl 20 US-09-732-561-21 Sequence 21, Appl 20 US-09-732-561-21 Sequence 21, Appl 20 US-09-732-561-21 Sequence 21, Appl 20 US-09-732-561-21 Sequence 21, Appl 20 US-09-732-561-21 Sequence 21, Appl 20 US-09-732-561-21 Sequence 21, Appl 20 US-09-732-561-21 Sequence 21, Appl 20 US-09-732-561-21 Sequence 21, Appl 20 US-09-732-561-21 Sequence 21, Appl 20 US-09-732-561-21 Sequence 21, Appl 20 US-09-732-561-21 Sequence 21, Appl 20 US-09-732-561-21 Sequence 21, Appl 20 US-09-732-561-21 Sequence 21, Appl 20 US-09-732-561-21 Sequence 21, Appl 21 US-09-732-561-21 Sequence 21, Appl 21 US-09-732-561-21 Sequence 21, Appl 21 US-09-732-561-21 Sequence 21, Appl 21 US-09-732-561-21 Sequence 21, Appl 21 US-09-732-561-21 Sequence 21, Appl 21 US-09-732-561-21 Sequence 21, Appl 21 US-09-732-561-21 Sequence 21, Appl 21 US-09-732-561-21 Sequence 21, Appl 21 US-09-732-561-21 Sequence 21, Appl 21 US-09-82-31 US-09-82-31 Sequence 21, Appl 21 US-09-82-31 US-09-82-31 Sequence 21, Appl 21 US-09-82-31 US-09-82-31 Sequence 21, Appl 21 US-09-82-31 US-09-82-31 Sequence 21, Appl 21 US-09-82-31 Sequence 21, Appl 21 US-09-82-31 US-09-82-31 Sequence 21, Appl 21 US-09-82-31 Sequence 21, Appl 21 US-09-82-31 Sequence 21, Appl 21 US-09-82-31 Sequence 21, Appl 21 US-09-82-31 Sequence 21, Appl 21 US-09-82-31 Sequence 21, Appl 21 US-09-82-31 Sequence 21, Appl 21 US-09-82-31 Sequence 21, Appl 21 US-09-82-31 Sequence 21, Appl 21 US-09-82-31 Sequence 21, Appl 21 US-09-82-31 Sequence 21, Appl 21 US-09-82-31 Sequence 21, Appl 21 US-09-82-31 US-09-82-31 Sequence 21, Appl 21 US-09-82-31 US-09-82-31 US-09-82-31 US-09-82-31 US-09-82-31 US-09-8
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ALIGNMENTS

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ESSULT. 12
Sequence 12, Application US/09829381A
Sequence 12, Application US/09829381A
Sequence 12, Application US/09829381A
Setent No. US20020144306A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yomines
Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for CORESPONDENCES: 20
CORESPONDENCES: 20
CORESPONDENCE ADDRESS:
ADDRESSEE: Charles B. Cohen, Monsanto Company, BB4F
STREET: 100 Chesterfield Village Parkway No. US20020144306A1th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
COMPUTER: READABLE FORM:
REDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/829,381A
FILING DATE: US-OPAT:-2001
CLASSIFICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNAY AGENT INFORMATION:
APPLICATION NUMBER: 34,565
REGISTRATION INFORMATION:
TELEPHONE: (314) 537-6224
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120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
                                                                                                                                                      181 ACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTGCCAGCTC
          61 TCTTTGCTGCTCTTGTTCTCTTTGCTGCCTTTTGAAGCACCAACAAAGGTGGAAGGT
                                                                                                                                                                                             181 ACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTGCCAGCTC
                                                                        9 GGATCCAAGAAAGTAATAGATATGGCTAAGTTTGCTACCATCATCTCTCTTTTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods
Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                       241 ACAAATGTATTTGTTACTTCCCATGTTAATAAGGATCCGAATTCCC
                                                                                                                                                                                                                                                                             241 ACAAATGTATTTGTTACTTCCCATGTTAATAAGGATCCGAATTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 38-21 (10700) A TELECOMMUNICATION INFORMATION: TELEPHONE: (314) 537-6224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-829-381A-14
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APPLICATION NUMBER: 09/103,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1998-06-24
ATTORNEY AGENT INFORMATION:
NAME: COhen, Charles E.
REGISTRATION NUMBER: 34,565
                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/09829381A
Patent No. US20020144306A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (314) 537-6047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCES: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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US-09-829-381A-14
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Sequence 12, Application US/10681972

Sequence 12, Application US/10681972

Publication Wo. US20040064850A1

SEQUENCE 11 Ang. US. US20040064850A1

APPLICANT: Liang. Jihong

APPLICANT: Snah, Dilip M.

APPLICANT: Rosenberger, Cindy A.

TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control TITLE OF INVENTION: Plant Pathogenic Fungi

CURRENT APPLICATION NUMBER: US/10/681,972

CURRENT PILING DATE: 2003-0-0.9

PRIOR PILING DATE: 2001-0-0.9

PRIOR PILING DATE: 1998-06-24

NUMBER: OSEQ ID NOS: 20

SEQ ID NO 12
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                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                   Length 286;
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100.0%; Pred. No. 8.7e-83;
rative 0; Mismatches 0;
                                                                                                                                                                                                                               100.0%; Score 286; DB 9;
100.0%; Pred. No. 8.7e-83;
iive 0; Mismatches 0;
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                                                                                                                                     ; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-829-381A-12
TELEFAX: (314) 537-6047
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                             TOPOLOGY: linear
ULE TYPE: CDNA
                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 286; Conservative
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Best Local Similarity 100.0
Matches 286; Conservative
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LENGTH: 286
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                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 Arcacadaaadraaradararddcraadrerechrechrencercerrerechecree
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                         Rosenberger, Cindy A.

TITLE OF INVENTION: Antifungal Polypeptide and Methods
Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                    CURPLET READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 ATCCAAGAAAGTAATAGATATGGCTAAGTTTGCTACCATCATCTCTCTT
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Pred. No. 5e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
NAME: COhen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: cDNA SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATITGTTACTTCCCATGTTAAT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/10681972
Publication No. US20040064850A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGIH: 500 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                         APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS
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91.68;
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Best Local Similarity 91.6'
Matches 241; Conservative
                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                     CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                            COUNTRY: USA
           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-829-381A-9
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US-10-681-972-9
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APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Contro;
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Contro;
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Contro;
TITLE OF INVENTION: Altifungal Polypeptide ALYAFP from Alyssum and Methods for Contro;
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/09/829,381D
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR PILLING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Version 3.1
SEQ ID NO 14
LENGTH: 270
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                                                           GCTCTTGTTCTTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCAAGGTTGTGCGAG 120
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                                                                                              AGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTCTTGTTCTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCAAGGTTGTGCGAG
GGATCCAASAAAGTAATAGWTATGGCTAAGTTTGCTACCATCATCTCTTCTTTTGCT
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Pred. No. 2.6e-77;
2; Mismatches 0; Indels
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US-10-681-972-14
; Sequence 14, Application US/10681972
; Publication No. US20040064850A1
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Patent No. US20020144306A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 99.3%;
Matches 268; Conservative
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; OTHER INFORMATION: Plasmid
US-10-681-972-14
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Sequence 5, Application US/10681972
; Sequence 5, Application US/10681972
; Publication No. US20040064850A1
; GENERAL INFORMATION:
APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Shah, Dilip M.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control
; TITLE OF INVENTION: Plant Pathogenic Fungi
; TITLE OF INVENTION: Plant Pathogenic Fungi
; TITLE OF INVENTION: Dane: 2003-10-09
; FILE REFERENCE: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/09/829,381D
; PRIOR APPLICATION NUMBER: 09/103,489
; PRIOR FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 20
; SEQ ID NO S: 20
; SEQ ID NO S
; LENGTH: 308
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                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apx-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.7%; Score 190.8; DB 9;
86.1%; Pred. No. 1e-51;
live 0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                 NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCED DOCKET NUMBER: 38-21 (10700) A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-829-381A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 308 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (314) 537-1
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 223; Conservative
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Best Local Similarity
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   APPLICANT: Liang Jihong
APPLICANT: Liang Jihong
APPLICANT: Liang Jihong
APPLICANT: Liang Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Wonnie, Tondy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Contro
TITLE OF INVENTION: Plant Pathogenic Fungi
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/09/829,381D
PRIOR APPLICATION NUMBER: US/09/829,381D
PRIOR FILING DATE: 2001-04-09
PRIOR FILING DATE: 2001-04-09
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 500
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ADDRESSE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 Arcacágaaagraaragararggcraagrargcriccarcarcriccrigicricrigic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 ATCCAAGAAAGTAATAGATATGGCTAAGTTTGCTACCATCATCTCTCTTCTTTGCTGC
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APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 216.6; DB 13; Length 500;
Pred. No. 5e-60;
0; Mismatches 19; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature

: LOCATION: (22)...(22)

: OTHER INFORMATION: N = any nucleotide

US-10-681-972-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATITGITACTICCCALGITAAT 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 91.6%;
Matches 241; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 63198
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Alyssum spp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-829-381A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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Gaps

79 65

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66 TTTTGCTGCTTTCGAAGCCCCAACAATGGTGGAAGCACAAAAGTTGTGCGAAAGGCCAAG 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 TGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGGTGACAAATGTATTTGTTA
                                                                                                                                                                                                                                                                                                                              20 AGTAATAGATATGGTAAGTTTGGTACGATCATCTGTTGTTGTTGGTGGTGTTTTGTTCT
                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                           Length 414;
                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                     Score 178.8; DB 9;
Pred. No. 9.7e-48;
0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: SUCHEFUL.

CURRENT APPLICATION NUMBER: US/10/388,361A

CURRENT FILING DATE: 2003-03-13

REIOR APPLICATION NUMBER: US 09/077,948

PRIOR FILING DATE: 1998-08-07

PRIOR FILING DATE: 1996-12-12

PRIOR FILING DATE: 1996-12-12

PRIOR FILING DATE: 1996-12-13

PRIOR FILING DATE: 1996-12-13

PRIOR FILING DATE: 1996-12-13

PRIOR FILING DATE: 1996-12-13

PRIOR FILING DATE: 1995-12-13

PRIOR FILING DATE: 1995-12-13

SURIOR FILING DATE: 1995-12-13

SURIOR FILING DATE: 1995-12-13

SURIOR FILING DATE: 1995-12-13

NUMBER OF SEQ ID NOS: 141

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Broekaert, Willem
APPLICANT: Van Gelder, Wilhelmus
APPLICANT: Rees, Sarah
TITLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: 50094PPDDIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 45, Application US/10388361A Publication No. US20030226169A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Borremans, Frans
Borremans, Frans
De Samblanx, Genoveva
Sitjtsma, Lolke
Meloen, Robbert
Puljk, Wouter
Schaaper, Wilhelmus
Broekaert, Wilhelmus
Van Gelder, Wilhelmus
                                                                                                                                                                                                                                                     62.5%;
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APPLICANT: Fant, Franky
          INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               257 CTTCCCATGTTAAT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246 crtrccrrcrrara
                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 84.3
Matches 214; Conservative
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; ORGANISM: Raphanus sativus
US-10-388-361A-45
202-822-0944
                                                                                                                                                                         CDS
16..255
                                                                                                                                                                     ; NAME/KEY;
; LOCATION:
US-09-759-584-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-388-361A-45
TELEFAX:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                 CAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAAATG 247
                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                       Length 308;
                                                                                                                                                                                 Score 190.8; DB 13; Length
Pred. No. 1e-51;
0; Mismatches 33; Indels
                                                                                                                                                                                                                                                               11 ATCCAAGAAAGTAATAGATATGGCTAAGTTTGCTACCATCATCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,584
    ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic PCR reaction product
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APPLICATION NUMBER: 08/377,687
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELEPHONE: 202-861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON
                                                             FEATURE:

NAME/KEY: misc feature

LOCATION: (22)...(248)

OTHER INFORMATION: N = any nucleotide
US-10-681-972-5
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MEDIUM TYPE: Floppy disk
COMPUTER: IBB PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 48, Application US/09759584
Patent No. US20010014732A1
GENERAL INFORMATION:
APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 TATTTGTTACTTCCCATGT 266
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                                                                                                                                                                                 66.78;
                                                                                                                                                                                                                      Matches 223; Conservative
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                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: D.C. COUNTRY: US. ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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US-09-759-584-48
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79 TCTTTGCTGCCTTTGAAGCACCACAATGGTGGATGCA---AGGTTGTGCGAGAGACAA 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGGGACATGGTCCGGAGTTTGCGGAAACAGTAACGCGTGCAAGAATCAGTGCATTAACC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 TTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAAATGTATTTGTT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 AAGTAATAGATATGCTAAGTTTGCTACCATCATCTCTCTTTCTCTTTGCTGCTCTTTGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 403;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732,561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 61.7%; Score 176.6; DB 9; Best Local Similarity 83.5%; Pred. No. 5e-47; Matches 213; Conservative 0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Peninock, IIIs
APPLICANT: Manners, John
APPLICANT: Manners, John
APPLICANT: Kemal
APPLICANT: Broekeart, Willem
IITLE OF INVENTION: Plant Protection Method
NUMBER OF SEQUENCES: 24
ADDRESSER: ZENECA AG Products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Hohenschutz, Liza D.
REGISTRATION UNMBRE: 33,712
REFERENCE/DOCKET NUMBER: PPD 50165/UST
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/01672
FILLING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, Liza D.
                                                                                                                                                                                                                 Sequence 13, Application US/09732561
Patent No. US20020035738A1
GENERAL INFORMATION:
APPLICANT: Thomma, Bart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/202,638
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1800 Concord Pike CITY: Wilmington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (302) 886-1699
INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
246 CTTTCCTTGTTAAT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: Sincl
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Thomma, Bart
APPLICANT: Terras, Franky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 19850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-732-561-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                               80 CTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGAGAGACCAAG 136
                                                                                                                                                                                                                                                                                                                                                                                                  66 ritrigcigcrircaaagcaccaacaardargaagcacagaagricigcgaaagcaaag 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAAATGTATTTGTTA 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65
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                                                                                                          3,
                           Query Match 62.5%; Score 178.8; DB 13; Length 414; Best Local Similarity 84.3%; Pred. No. 9.7e-48; Matches 214; Conservative 0; Mismatches 37; Indels 3;
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Publication No. US20020152498A1

GEMERAL INFORMATION:
APPLICANT: De Samblanx, Genoveva
APPLICANT: Broekaert, Willem
APPLICANT: Broekaert, Willem
APPLICANT: Reses, Sarah
ITLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: SYN-034DV
CURRENT APPLICATION NUMBER: US/10/006,252A
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/077,951
PRIOR APPLICATION NUMBER: GB 9525474.4
PRIOR APPLICATION NUMBER: PCT/GB96/03065
PRIOR APPLICATION NUMBER: PCT/GB96/03065
PRIOR APPLICATION NUMBER: PCT/GB96/03065
PRIOR FILING DATE: 1996-12-13
PRIOR FILING DATE: 1996-12-13
SPRIOR FILING DATE: 1996-12-13
SOFTWARE PRIOR FILING DATE: 1996-12-13
NUMBER OF SEQ 1D NOS: 77
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US-10-006-252A-19
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Best Local Similarity 84.3
Matches 214; Conservative
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US-10-006-252A-19
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LENGTH: 414
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APPLICANT: Chang, H.
APPLICANT: Chang, H.
APPLICANT: AN, T.
APPLICANT: Han, Y.
APPLICANT: Hang, X.
APPLICANT: Wang, X.
APPLICANT: Cooper, Bret
TITLE OF INVENTION: Promoters for regulation of plant expression CURRENT APPLICATION WINDER: US/09/887,576
CURRENT APPLICATION WINDER: US/09/887,576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 400;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US/U9/887,576

PRIOR APPLICATION NUMBER: US 60/213,848

PRIOR FILING DATE: 2000-06-23

PRIOR PRILING DATE: 2000-06-23

PRIOR PILING DATE: 2000-06-23

PRIOR PILING DATE: 2000-06-23

PRIOR PILING DATE: 2000-16-29

NUMBER OF SEQ ID NOS: 875

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 607

LENGTH: 400
                                                                                                                                                                                                                                                                                               Sequence 607, Application US/09887576
Patent No. US20020144047A1
GENERAL INFORMATION:
APPLICANT: Budworth, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)...(400)
; OTHER INFORMATION: n = A,T,C or
US-09-887-576-607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                     257 CTTCCCATGTTAA 269
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US-09-759-584-58
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80 CTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGAGAGAGACAAG 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732,561
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 176.2; DB 9;
Pred. No. 6.7e-47;
0; Mismatches 38;
                                                                                                                                                                                                  Sequence 15, Application US/09732561
Patent No. US20020035738A1
GENERAL INPORMATION:
APPLICANT: Thomms Bart
APPLICANT: Penninckx, Iris
APPLICANT: Manners, John
APPLICANT: Manners, John
APPLICANT: Manners, John
APPLICANT: Manners, John
APPLICANT: Manners, John
APPLICANT: Manners, John
APPLICANT: Broekaert, Willem
TITLE OF INVENTION: Plant Protection Method
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATJORNEJ/MAENA LARLOMENTO.

RAGISTRATION NUMBER: 33,712

REFERENCE/DOCKET NUMBER: PPD 50165/UST

TELECOMMUNICATION INFORMATION:

TELEPHONE: (302) 886-1699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/01672
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/202,638
                                                                                                                                                                                                                                                                                                                                                                                                                                                SSEE: ZENECA AG Products
: 1800 Concord Pike
Wilmington
                                                               256 ACTICCCAIGITAAT 270
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Best Local Similarity 83.8%;
Matches 212; Conservative
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TYPE: nucleic acid
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ORIGINAL SOURCE:
STRAIN: PDF1.2
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STREET: 18
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US-09-732-561-15
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STATE: DI
COUNTRY:
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80 CTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGAGAGACCAAG 136
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         Sequence 58, Application US/09759584 Patent No. US20010014732A1
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; LOCATION:
US-09-759-584-58
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Search completed: May 18, 2004, 20:33:21 Job time : 264.25 secs

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Email: singhja@em.agr.ca.
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CB263345 25-EB974-
CD834068 BN45.040H
CD832592 BN40.0630
                                                                   May 18, 2004, 17:05:11; Search time 2381.6 Seconds (without alignments) 3586.070 Million cell updates/sec
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                                                                                                                US-10-681-972-12
286
1 gggaattcggatccaagaaa......taataaggatccgaattccc 286
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                                                                                                                                                                                                                                55026578
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                     27513289 seqs, 14931090276 residues
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Maximum Match 100%
Listing first 45 summaries
                                             OM nucleic - nucleic search, using sw model
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CD834068
CD832592
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em_gss_pln: *
em_gss_pln: *
em_gss_vrt: *
em_gss_vrt: *
em_gss_vrt: *
em_gss_mm: *
em_gss_mm: *
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Maximum DB seq length: 200000000
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em_gss_rod:*
em_gss_phg:*
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gb_gssl:*
gb_gss2:*
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em_esthum:*
em_estin:*
em_estov:*
em_estpl:*
em_estpl:*
em_htc:*
gb_est1:*
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Match Length DB
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gb_htc:*
gb_est3:*
gb_est4:*
gb_est5:*
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Perfect score:
                                                                                                                                                                  Scoring table:
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177.8
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                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                           Sequence:
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                                                                    Run on:
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No.
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	2	77.8	62.2	452	14	4 CD832071		D83207	BN40.0610
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	-	77.2		394	12	BG32145		EG321454	DS01 ORPO
υ	96	76.6		422	σ,	AV787956		.V787956	AV787956
1 -	1.	70.7		400 408	4 4	T04323		T04323 3	70 Lambda-
ı	7	76.2		409	14	CD83409		CD833779	BN45.0011
ri r	m ·	76.2		420	14	CD83394		CD833944	BN45.040B
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iĀ	11	76.2	61.6	421	14	CD83397		CD831111	BN40.058A BN45.040D
н,		76.2		422	14	CD83398		CD833983	BN45.040D
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8		76.2		438	14	CD83147		CD831479	BN40 059.T
CA C	11.	76.2		450	14	CD83461		CD834611	BN45.042H
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1 (3	2 4.	175		421	1 6	AV816118		VR16118	LTS1949 Pe
Ü	ın.	175		422	0	AV788559		V788559 7	4V788559
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'nñ	- r	74.6		419	14	CD83416		CD834168	BN45.040N
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ë	0	74.6		519	14	CD835064		CD835064	BN45 040E
m i	-1	173		421	14	CD837517		CD837517	BN45.052I
m 'n	o o	173		422	14	CD831972		CD831972	BN40.0611
ήď	n 4	173		424	4.4	CD833048		CD833048	BN40.065M
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4, 4	N 4	166		457	44.	CD831226		CD831226	BN40.058J
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SOURCE		Desc	uraini	a sophi	rd				
ORG	GANISM	Desc	uraini	a sophi	ه ا ا	į	-	-	
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AUTHORS		Sing	h, J.A.,	Piche	; ن	uroux	P., De Moors, A., H	rris	
TITLE		Hatt	ori,ï.] essed	I., Oue	llet P Ta	, Rob	rt,L.S., Sprott,D.	and	Finker, N.A.
i		Seed	lings	5)) .		מומים הטומים העם	arme	pina
COMMENT		Cont	blished act: Sj	1 (2001 Ingh,J.	~ A				
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		X X	eatby E	31dg., C	Cent	ral Exper	mental Farm, Ott	awa, Ontario	io, KlA
		9 G	(613)	1 759-16	ć				
		Fax:	(613)	759-17	7 10				
		Kma.	4.5	mo@er4x	,	ĺ			

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/tlssue_type="seedling"
/dev_tstage="few_days old seedlings"
/lab_host="E. coil 'IL-Blue MRF"
/clone lib="WRIZ-ADIS-008"
/note="Vector: pBluescript SK (-); Site 1: EcoRI; Site 2:
Xho1; cDNA library from Arabidopsis thaliana, accession
C24; seedling; Lambda ZAPII phage library was made at the
Max-Planck-Institute of Molecular Plant Physiology, Golm,
Germany and mass-excised at the Max-Planck-Institute for
Plant Breeding Research, Cologne, Germany; cloning sites
EcoRI-Xho1; Mote: Sequencing granted in the context of the
GABI Arabidopsis Verbund I: Genetic Diversity,
'Establishment of Migh-efficiency SNP-based mapping tools
and development of methods for genome-wide mutation
detection PI: Bernd Weisshaar Sequence submission managed
by RZEDF/GABI-Primary database: http://gabi.rzpd.de This
clone is available from RZPD; contact RZPD (clone@rzpd.de)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD834068 446 bp mRNA linear EST 10-JUL-2003
BN45.040H17F011019 BN45 Brassica napus cDNA clone BN45040H17, mRNA
sequence.
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Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
Genoplante
Genoplante
33, rue Henri Rochefort 91025 BVRY CEDEX France
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15 AATAATCATCATGGCTAAGTTTGCTTCCATCATCACCTTATCTTGGCTGCTCTTGTTCT
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62.2%; Score 177.8; DB 14; Length
Best Local Similarity 84.2%; Pred. No. 6e-38;
Matches 213; Conservative 0; Mismatches 37; Indels
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                 Location/Qualifiers
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JOURNAL
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                                                                                                                                                                /clone="D801 0806"
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/dev_stage="1-month seedlings - 1 cm tall - 8 leaf"
/clone_lib="D801_AAFC_ECORC_cold_stressed_Flixweed_seedlin
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25-E8974-008-017-A07-pB12 MPIZ-ADIS-008 Arabidopsis thaliana cDNA clone MPIZp767A0717Q 5-PRIME, mRNA sequence.
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Large-scale identification and analysis of genome-wide single-nucleotide polymorphisms for mapping in Arabidopsis thaliana Genome Res. 13 (6), 1250-1257 (2003)
                                                                                                                                                                                                                                                                                                                                        /note="Vector: Bluescript SK+/Xhol-EcoRI; Site 1: Eco RI; Site 2: Xho I; Plants were grown for 1 month at 200C/16 site I:ght/day (average 8 leaves, 1 cm tall, weight 0.02g/plant). Then they were exposed to 20C, 12 hrs light/day, for 1 week. Library prepared by C. Piche using Stratagene kit."
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42; Indels
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ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
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Fax: 00492215062851
                                                                       organism="Descurainia sophia"
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Insert Length: 41 std Error: 0.00
Plate: 17 row: A column: 07
Seg primer: pBl2; GGTGGGGGGCGCTCTAG.
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                                                                                                   /mol_type="mRNA"
/db_xref="taxon:89411"
   location/Qualifiers
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Matches 20
                                       source
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Gaps 3;

DB 14; Length 441;

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EST 10-JUL-2003
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BN40.061003F011227 BN40 Brassica napus cDNA clone BN40061003, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brassica napus (rape)
Brassica napus
Brassica napus
Brassica napus
Brassicanapus
Brassicanalophyta; Euclichyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                             93, rue Henri Rochefort 91025 EVRY CEDEX France
Tal: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
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Unpublished (2003)
Contact: Genoplante
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                                                                                                                                                                                                                                                                  115 TITCGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAAGAGCCCAAG
                                                                                                                                                                                                                                                                                                                  137 IGGGACAIGGICAGGAGITIGIGGGAACAACAATGCAIGCAGGAACCAAIGCAGAAACCI
                                                                                                                                                                                                                                                                                                                                                     175 TGGGACATGGTCTGTGGAAACAATAACGCATGCAAGAATCAGTGCATTAACCT
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                                                                                                                                 37; Indels
                                                                                            Score 177.8; DB 14;
Pred. No. 6e-38;
0; Mismatches 37;
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84.2%; Pred. No. 6e-38;
Mismatches 37;
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/clone="BN40061003"
               /tissue_type="seed"
/clone_lib="BN40"
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/clone_lib="BN40"
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                                                                                          62.2%;
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                                                                                                         Best Local Similarity 84.2
Matches 213; Conservative
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                                                                                            Query Match
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core eudicots;
Tosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 447)
                                                                                                                                                                                                                                                                                                                                                                                            79
Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).

Location/Qualifiers
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Unpublished (2003)
Contact: Genoplante
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Location/Qualifiers
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                                                                                                                   1. .446
/organism="Brassica napus"
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/cultivar="Jet neuf"
/db_xref="Laxon:3708"
/clone="BN45040H17"
/fissue_type="seed"
/clone_lib="BN45"
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/clone="BN40063015"
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CD832592.1 GI:32514532
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Best Local Similarity 84.2%;
Matches 213; Conservative (
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Fax: 33 1 69 47 54 10
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CD831680 470 bp mRNA linear EST 10-JUL-2003 BN40.060H13F011227 BN40 Brassica napus cDNA clone BN40060H13, mRNA
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DS01_08h05_A DS01_AAFC_ECORC_cold_stressed_Flixweed_seedlings
Descurainia sophia cDNA clone DS01_08h05, mRNA sequence.
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Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trac
Spermatophyta; Magnoliophyta; eudicotyledons; core eudico
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 470)
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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62.2%; Score 177.8; DB 14;
Best Local Similarity 84.2%; Pred. No. 6e-38;
Matches 213; Conservative 0; Mismatches 37;
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/db_xref="texon:3708"

clone="BN40060H13"

/tissue type="seed"

clone_lib="BN40"
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CD831680.1 GI:32513620
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Genoplante
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BN45.043006F011229 BN45 Brassica napus CDNA clone BN45043006, mRNA sequence.
                   TITCGCTGCTTTCGAAGCACCAACAATGGTGGAAGCACAGAAGTTGTGCGAGAGGCCAAG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
peparantophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
(bases 1 to 458)
CTITGCTGCCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGAGAGACCAAG 136
                                                                                                                                         TGAAAGAGAGAACACGGATCTTGCAACTATGTCTTCCCAGGTCACAAATGTATTTGTTA 256
                                                                                                                                                                                 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTAGTGAGCATGGCTAAGTTTGCTTCATTGCCCCACTTTTTGCTGCTCTTGTTCT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 CTTTGCTGCCTTTGAAGCACCAAAAATGGTGGATGCA---AGGTTGTGCGAGAGAGAAGA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGAAAGAGCAGAACCACGGATCTTGCAACTATGCTTCCCAGCTCACAATGTATTTGTTA 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genoplante, a major partnership french program in plant genomics Unpublished (2003)
                                                                    180 TGGGACATGGTCAGGAGTCTGTGGGAACAATAACGCATGCAAGAATCAGTGCATTAACCT
                                                                                                                                                                           240 reaganageaceacardearcriceaacrarerriceaacracacracaagrarrigera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .458
| /organism="Brassica napus"
| /organism="Brassica napus"
| /orditivar="Jet neuf"
| /db_xref="taxon:3708"
| /clone="By45043006"
| /tissue_type="seed"
| /clone_lib="BN45"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  CD834994.1 GI:32516934
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brassica napus (rape)
Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Genoplante
Genoplante
                                                                                                                                                                                                               CTTCCCATGTTAA 269
                                                                                                                                                                                                                                                     CTTCCCTTGTTAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 84.2
Matches 213; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genoplante.
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80
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                                                                  137
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CD834994
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center

73-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: meski@rtc.riken.go.jp
Email: meski@rtc.riken.go.jp
Brabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a modified pBluescript vector as a Sstl/Khol insert. Please visit our further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T04323 400 bp mRNA linear EST 06-NOV-1997 370 Lambda-PRL2 Arabidopsis thaliana CDNA clone 37F10T7, mRNA sequence.
                                                                                      Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itch,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Sparmatophyta, Magnoliophyta, eudicotyledons, core eudicots; rosids, eurosids II; Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGAGAGACCAA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTTTGCTGCTCTTGAAGCACCGATGGTGGTGGAAGCACAGAAGTTGTGCGAGAGGCCCAA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 GIGGGACAIGGICAGGAGITIGIGGGAACAACAAIGCAIGCAGGAACCAAIGCAGAAACC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 TTGAGAAAGCACGACATGTTGCAACTATGTCTTCCCAGCTCACAATGTATCTGCT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="plants at various developmental stages from germination to mature seeds" /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    272 Gradakardrandarinacagaahaakarakardagaadahaarakardardarahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 TIGAAAGAGCAGAACACGGATCTIGCAACIAIGICIICCCAGCTCACAAAIGIAITIIGIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                               Large scale analysis of Arabidopsis full-length cDNA (2002b) Unpublished (2002)
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/note="Site_1: SstI; Site_2: XhoI; subjected the advoration" [1, 2, 5, 10, 24 hr) and cold (1, hr) treatments"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tch 61.7%; Score 176.6; DB 9;
al Similarity 83.5%; Pred. No. 1.3e-37;
213; Conservative 0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="RAFL06-77-K06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256 ACTICCCAIGITAAT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T04323
T04323.1 GI:315483
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Best Local Si
Matches 213;
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JOURNAL
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                                                                                          AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db xref="taxon:89411"
/db xref="taxon:89411"
/dlone="1001_08h05"
/tissue type="leaf, stem"
/dev_stage="1-month seedlings - 1 cm tall - 8 leaf"
/dlone_lib="D801_AAFC_ECORC_cold_stressed_Flixweed_seedlin
                                   Descurainia sophia

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Descurainia.

1 (bases 1 to 394)

Sigh, J.A., Piche, C., Couroux, P., De Moors, A., Harris, L.J.,
Hattori, J.I., Ouellet, T., Robert, L.S., Sprott, D. and Tinker, N.A.
Bxpressed Sequence Tags from Cold-Stressed Descurainia sophia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: Eco RI; Site 2: Xho I; Plants were grown for 1 month at 200C/16 hrs light/day (average 8 leaves, 1 cm tall, weight 0.02g/plant). Then they were exposed to 2oC, 12 hrs light/day, for 1 week. Library prepared by C. Piche using Stratagene kit."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTTTGCTGCCTTTGAAGCACCAACAATGGTGGATGCA---AGGTTGTGCGAGAGACCAAG 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78
                                                                                                                                                                                                                                                    Contact: Singh,J.A.

Bastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, KlA
CG. Canada
Tel: (613) 759-1662
Fax: (613) 759-1701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCAGCTCACAAATGTATTTGTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 AGTAATAGATATGGCTAAGTTTGCTACCATCATCTCTCT

    .394
    /organism="Descurainia sophia"

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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                    Bmail: singhja@em.agr.ca.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:19806746
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                   Descurainia sophia
                                                                                                                                                                                                                                Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213; Conservative
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AV787956
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Matches 21
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KEYWORDS
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AV787956/c
LOCUS
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                                                                                                                                              AUTHORS
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Tracheophyta;

Brassica napus (rape)
Brassica napus
Brassica napus
Brassica napus
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheor
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

Genoplante.

93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante.info.infobiogen.fr).

Location/Qualifiers

FEATURES

L. .408

Genoplante, a major partnership french program in plant genomics Unpublished (2003) Contact: Genoplante

Genoplante

REFERENCE AUTHORS TITLE JOURNAL COMMENT

SOURCE ORGANISM

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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 400).

Newman, T., deBruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, C. Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                              Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 61.6%; Score 176.2; DB 14; Length 400; Best Local Similarity 83.8%; Pred. No. 1.6e-37; Matches 212; Conservative 0; Mismatches 38; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 AGTAATAGATATGGCTAAGTTTGCTACCATCATCTCTCTTTTGC
                                                                                                                                                                                                                                                                     Email: 22313tcn@ibm.cl.msu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oligo dT primed cDNA.
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Location/Qualifiers
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Fax: 517-353-9168
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409 bp mRNA linear EST 10-JUL-2003 BN45.040121F011018 BN45 Brassica napus cDNA clone BN45040121, mRNA CDB34090 CDB34090.1 GI:32516030
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Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France
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Best Local Similarity 83.8%; Pred. No. 1.6e-37;
Matches 212; Conservative 0; Mismatches 38
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CD833779 408 bp mRNA linear EST 10-JUL-2003 BN45.001115F010914 BN45 Brassica napus CDNA clone BN45001115, mRNA

GI:32515719

sequence. CD833779 CD833779.1 EST.

ACCESSION VERSION KEYWORDS

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CD826491 421 bp mRNA linear EST 10-JUL-2003
BN25.064A05F020416 BN25 Brassica napus CDNA clone BN25064A05, mRNA
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Brassica napus
Brassica napus
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II, Brassicales; Brassicaceae; Brassica.

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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
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Matches 212; Conservative 0; Mismatches 38; Indels 3;
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Matches 212; Conservative 0; Mismatches 38.
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CD826491.1 GI:32508431
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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Contact: Genoplante
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            Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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Best Local Similarity 83.8%; Pred. No. 1.6e-37;
Matches 212; Conservative 0; Mismatches 38
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Search completed: May 18, 2004, 19:00:29 Job time : 2384.6 secs

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GenCore version 5.1.6

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	OM nucleic - nucleic search, using sw model	Run on: May 18, 2004, 16:14:01; Search time 757.05 Seconds (without alignments) 8816.891 Million cell updates/sec	Title: US-10-681-972-12_COPY_116_269 Perfect score: 154 Sequence: 1 aaggttgtgcgagagaccaatttgttacttcccatgttaa 154	Scoring table: IDENTITY NUC Gapop 10-0 , Gapext 1.0	Searched: 3470272 segs, 21671516995 residues	Total number of hits satisfying chosen parameters: 6940544	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : GenEmbl:* 1
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	0.000000000000000000000000000000000000	AX50067 Sequence BD174927 Disease t AX13787 Arabidops U1857 Raphanus sa A66874 Sequence 15 A26875 R. sativus A A39549 Sequence 19 A63404 Sequence 19 AR050153 Sequence B31545 Antibacteri	linear PAT 05-DEC-1998 and Rosenberger, C. Annette.
SUMMARIES ID	ARA12239 ARA32391 ARA32399 ARA32399 ARA32389 ARA32389 ARA132389 ARA132389 BV010406 BV010709 BV010700 BV010700 BV010703 ARA12601 AXA12601 AXA12601 AXA12601 AXA12601 AXA12601 AXA12601 AXA12601 AXA12601 AXA12601 AXA12601 BV010671 BV010671 BV010671 BV010671 BV010673	AXS90057 BD174927 AY137927 AY137927 AY137927 ASG8647 AG8647 A39549 A33549 A33549 A31545 AR130272 B31545 ALIGNMENTS	270 bp DNA 45 45 anlal., Wu,Y.Shun. 14 30-JUN-1998;
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Liang, J., Shah, D.M., Wu, Y.S. and Rosenberger, C.A.
Intifungal polypeptide AlyArp from Alyssum and methods for
controlling plant pathogenic fungi
Patent: US 6653280-A 12 25-NOV-2003;
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ilarity 100.0%; Pred. No. 3.8e-36;
Conservative 0; Mismatches 0;
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100.0%; Pred. No. 3.8e-36;
ive 0; Mismatches 0;
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                              Patent: US 5773696-A 12 30-JUN-1998;
Location/Qualifiers
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AR432389
AR432389.1 GI:40194666
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AR014686.1 GI:3972140
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1 (bases 1 to 286)
Liang,J., Shah,D.Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette.
                                                                                                                                                     1 AAGGITGIGCGAGACCAAGIGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG
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1 (bases 1 to 270)

Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.

Antifungal polypeptide AlyAFP from Alyssum and methods for controlling plant pathogenic fungi
Patent: US 6653280-A 14 25-NOV-2003;
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Best Local Similarity
Matches 134; Conserv
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           1 (bases 1 to 500)
Liang,J., Shah,D.Maganlal., Wu,Y.Shun. and Rosenberger,C.Annette.
Antifungal polypeptide and methods for controlling plant pathogenic
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MASC_STS16442 Arabidopsis thaliana (Landsberg erecta accession)
genomic DNA Arabidopsis thaliana STS genomic, sequence tagged site.
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Liang, J., Shah, D.M., Wu, Y.S. and Rosenberger, C.A.
Antifungal polypeptide AlyAPP from Alyssum and methods for
controlling plant pathogenic fungi
Patent: US 6653280-A 9 25-NOV-2003;
Location/Qualifiers
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                                                                                                                                                                       Length 500;
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Pred. No. 6.1e-32;
0; Mismatches 8; Indels 0
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                                                                                                                                                                       DB 6;
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                                                                                                                                                                 91.0%; Score 140.2; DB 6
94.8%; Pred. No. 6.1e-32;
ive 0; Mismatches 8
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/mol_type="unassigned DNA"
                                                                  Patent: US 5773696-A 9 30-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9 from patent US 6653280. AR432386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AR432386.1 GI:40194663
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94.8%;
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Best Local Similarity 94.8
Matches 145; Conservative
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Matches 145;
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Best Local 8
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ACCESSION

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/mol_type="genomic DNA"
/strain="Landsbarg erecta"
/db_train="Landsbarg erecta"
/db_train="Landsbarg erecta"
/db_train="landsbarg erecta"
/clone lib="Arabiioposis thaliana (Landsberg erecta
accession) genomic DNA"
/note="Genomic DNA prepared from rosette leaves. DNA was
amplified and directly sequenced from both directions and
assembled into a consensus sequence. Note: Sequencing
granted in the context of the GABI Arabidopsis VerbundI:
Genetic Diversity, 'Establishment of high-efficiency
SNP-based mapping tools and development of methods for
genome-wide mutation detection' PIS: Thomas Altmann,
Thomas Mitchell-Olds, Bernd Weisshaar"
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 526)
Schmid, K.J., Sorensen, T.R., Stracke, R., Torjek, O., Altmann, T.,
Idrichil-Jolds, T. and Weisshaar, B.
Large-Scale Identification and Analysis of Genome-Wide
Single-Nucleotide Polymorphisms for Mapping in Arabidopsis thaliana
Genome Res. 13 (6), 1250-1257 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 degrees for 2.00 minute(s) 94 degrees for 0.50 minute(s) 58 degrees for 0.50 minute(s) 72 degrees for 1.00 minute(s) 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Chemical Ecology
                                                                                                                                                                                                                                                                                                                                                    Synonyms: PCP16C2_ler.a
Contact: Karl Schmid
Department of Genetics and Evolution
Max-Planck-Institute of Chemical Ecology
Winzerlaer Str. 10, 07745 Jena, Germany
Tel: + 49-3641-571465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Taq Polymerase: 0.05 units/ul
Total Vol: 10 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer A: CGCTGCTCTTGTTCTCTTTG
Primer B: AAACAACCGTTGTTGGTCA
STS size: 526
PCR Profile:
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each 400 uM
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Location/Qualifiers
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each 1 uM
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KCl: 50 mM
Tris-HCl: 10 mM
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PCR Cycles:
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core endicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
I (bases I to 575)
Schmid,K.J., Sorensen,T.R., Stracke,R., Torjek,O., Altmann,T.,
Mitchell-Olds,T. and Weisshaar,B.
Large-Scale Identification and Analysis of Genome-Wide
Single-Nucleotide Polymorphisms for Mapping in Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BV010710 575 bp DNA linear STS 18-JUL-2003 MASC_STS16443 Arabidopsis thaliana (Weiningen-0 accession) genomic DNA Arabidopsis thaliana STS genomic, sequence tagged site.
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                                                                                                                                                                       Gaps
                  Thomas Altmann
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0
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                                                                                                                     Score 122.6; DB 11; Length
Pred. No. 1.4e-26;
0; Mismatches 19; Indels
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             genome-wide mutation detection' PIs: T
Thomas Mitchell-Olds, Bernd Weisshaar"
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PON Cycles: 35
Thermal Cycler: Perkin Elmer Geneamp9600
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Contact: Karl Schmid
Department of Genetics and Evolution
Max-Planck-Institute of Chemical Ecology
Winzerlaer Str. 10, 07745 Jena, Germany
Tel: +49-3641-571465
Fax: +49-3641-571405
Fmail: schmid@ice.mpg.de
Primer A: CGCTGCTCTTGTTCTCTTTG
Primer B: AAACAAACGTTGTTCTTTTG
FTS size: 575
PCR Profile:
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Total Vol: 10 ul
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BV010710.1 GI:32963208
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Best Local Similarity 87.6%;
Matches 134; Conservative
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50 mM
10 mM
8.3.
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KCl: 5
Tris-HCl: 1
PH: 8
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                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Late Cless)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 574)
Schmid, K.J., Sorensen, T.R., Stracke, R., Torjek, O., Altmann, T., Mitchell-Olds, T. and Weisshaar, B.
Large-Scale Identification and Analysis of Genome-wide Single-Nucleotide Polymorphisms for Mapping in Arabidopsis thaliana 22683290
                                                                                                                                                                                                                    BV010696 574 bp DNA linear STS 18-JUL-2003 MASC STS16441 Arabidopsis thaliana (Eifel-2 accession) genomic DNA Arabidopsis thaliana STS genomic, sequence tagged site.
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102 AAGAATCAGTGCATTAACCTTGAAGGAGCAAAACATGGATCTTGCAACTATGTCTTCCCA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana (Eifel-2 accession)
genomic_DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 degrees for 2.00 minute(s) 94 degrees for 0.50 minute(s) 58 degrees for 0.50 minute(s) 72 degrees for 1.00 minute(s)
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PCN Cycles: 35
Thermal Cycler: Perkin Elmer Geneamp9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synonyms: PCP16C2_ei2.a
Contact: Karl Schmid
Department of Generics and Evolution
Max-Planck-Institute of Chemical Ecology
Winzerlaer Str. 10, 07745 Jena, Germany
Tel: + 49-3641-571465
Fax: + 49-3641-571465
Email: schmid@ice.mpg.de
Primer A: CGCTGCTCTTGTTCTCTTTG
STISSIZE: 574
PCR. PROfile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1..574
Corganism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Eifel-2"
                                                                 122 GCTCACAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                        162 GCTCACAAGTGTATCTGTTACGTCCCATGTTAA 194
                                                                                                                                                                                                                                                                                                                                 STS.
Arabidopsis thaliana (thale cress)
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Primer: each 1 uM
dNTPs: each 400 uM
Tag Polymerase: 0.05 units/ul
Total Vol: 10 ul
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BV010696.1 GI:32963194
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Template:
Primer:
dNTP8:
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MgCl2:
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BV010696/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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COMMENT

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1 (bases 1 to 602).
Schmid, K.J., Sorensen, T.R., Stracke, R., Torjek, O., Altmann, T.,
Mitchell-Olds, T. and Weisshaar, B.
Large-Scale Identification and Analysis of Genome-Wide
Single-Nucleotide Polymorphisms for Mapping in Arabidopsis thaliana
Genome Res. 13 (6), 1250-1257 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Abstract = Lecoux/Puy-de-Dome-On-

/Glone lib="Arabidopsis thaliana (Lezoux/Puy-de-Dome-On-

accession) genomic DNA"

/note="Genomic DNA prepared from rosette leaves. DNA was

amplified and directly sequenced from both directions and

assembled into a consensus sequence. Note: Sequencing

granted in the context of the GABI Arabidopsis VerbundI:

Genetic Diversity, 'Establishment of high-efficiency

SPNP-based mapping tools and development of methods for

groome-wide mutation detection' PIS: Thomas Altmann,

Thomas Mitchell-Olds, Bernd Weisshaar"
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DNA Ārabidopsis thaliana STS genomic, sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       426 AAGAATCAGTGCATTAACCTTGAAGGAGCAAAACATGGATCTTGCAACTATGTCTTCCCA 367
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA
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                                        Thermal Cycler: Perkin Elmer Geneamp9600
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/mol_type="genomic DNA"
/strain="Lezoux/Puy-de-Dome-0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 79.6%; Score 122.6; DB 1:
Best Local Similarity 87.6%; Pred. No. 1.4e-26;
Matches 134; Conservative 0; Mismatches 19
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                                                            .c.wp.rate: 20 - 100 ng
Primer: each 1 uM
dNTPs: each 400 uM
Taq Polymerase: 0.05 units/ul
Total Vol: 10 ul
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Contact: Karl Schmid
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KCl: 50 mM
Tris-HCl: 10 mM
pH:
                    PCR Cycles:
                                                                    Protocol:
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Large-Scale Identification and Analysis of Genome-Wide
Single-Nucleotide Polymorphisms for Mapping in Arabidopsis thaliana Genome Res. 13 (6), 1250-1257 (2003)
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                                                                                                                                                                                                     Juote="Genomic DNA prepared from rosette leaves. DNA was amplified and directly sequenced from both directions and assembled into a consensus sequence. Note: Sequencing granted in the context of the GABI Arabidopsis Verbund: SNP-based mapping tools and development of high-efficiency genome-wide mutation detection, Pis: Thomas Altmann, Thomas Mitchell-Olds, Bernd Weisshaar"
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Makaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Wagnollophyta, eudicotyledons, core eudicots;
rosids, eurosids II, Bassicales, Brassicaceae, Arabidopsis.

1. (bases 1 to 578)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 AAGTIGIGGGAGAAGCCAAGIGGIACITIGGICAGGAGITIGCGGAAACAGCAAIGCAIGC 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 AAGAATCAGTGCATTAACCTTGAAGGAGCAAAACATGGATCTTGCAACTATGTCTTGCCA 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                     /db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana (Weiningen-0 accession)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 79.6%; Score 122.6; DB 11; Length 575; Best Local Similarity 87.6%; Pred. No. 1.4e-26; Matches 134; Conservative 0; Mismatches 19; Indels 0;
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s for 0.50 minute(s)
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                                                               organism="Arabidopsis thaliana"
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Department of Genetics and Evolution
Max-Planck-Institute of Chemical Ecology
Winzerlaer Str. 10, 07745 Jena, Germany
Tel: + 49-3641-571462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
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                                                                                type="genomic DNA"
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94 degrees 1
58 degrees 1
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Primer A: CGCTGCTCTTGTTCTTG
                                                                                                            /strain="Weiningen-0"
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Location/Qualifiers
1. .575
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BV010700.1 GI:32963198
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Annealing:
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PCR Profile:
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               FEATURES
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Gaps 0, 61

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Direct Submission

Submitted (26-MG-1998) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-6812, Japan (E-mail:ynakamu@kazusa.or.jp,
Tel: 61-438-52-3335, Fax: 81-438-52-3944)
Address for correspondence: Raos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MFCi6
Genes with similarity to proteins in the databases are described in
'product' or 'note' qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.
The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGenes (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
thtp://genome.wustl.edu/eddy/tRNAscan-SE
floam Eddy, Washington University School of this clone. It may be
shorter Decause we remove overlaps between neighboring submissions.
The 5' clone is K912 and the 3' clone is K15C23.
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LDRQCMGEDFFWAIRGGGGSSFSVVLSWKIRLLDVPSVVTVFKVVKTSEKEAVSIINK
WQYIADKVPNDLFIRAMLQKETEVYASFPGLYLGPVSDLLALMKDKFPELGLEIGNCR
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LHGIHIRTRSGGHDYEGLSYMAKSRPFVVIDLRNLRSITLDVDNRTGWVQSGATIGEL
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                                                                                                     Kaneko,T., Katch,T., Sato,S., Nakamura,Y., Asamizu,E., Kotani,H., Miyajima,N. and Tabata,S.
Structural analysis of Arabidopsis thaliana chromosome 5. IX.
Sequence features of the regions of 1,011,550 bp covered by seventeen Pl and TAC (alones
DNA Res. 6 (3), 183-195 (1999)
                      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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/product="berberine bridge enzyme-like protein"
/protein_id="BAB09147.1"
/db_xref="GI:9758693"
  Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="berberine bridge enzyme"
/note="CDS is reported in Acc# AB011475
gene_id:K9L2.20"
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complement(1020...1516)
/product="berberine bridge enzyme"
/note="CDS is reported in Acc# AB011475
gene_id:K9L2.20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'organism="Arabidopsis thaliana"
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complement(4691..6298)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="gene_id:MFC16.3"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic_DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="MFC16"
/clone_lib="Mitsui P1"
complement(1. .926)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome="5"
                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 61290)
Nakamura, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             number=2
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JOURNAL
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                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                         MEDLINE
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                                                                                                                                                                                                                                                JOURNAL
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                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABUL7065 ALALiana genomic DNA, chromosome 5, Pl clone:MFC16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Juctes General DNA prepared from rosette leaves. DNA was amplified and directly sequenced from both directions and sassembled into a consensus sequence. Note: Sequencing gratted in the context of the GABI Arabidopsis Verbund: Genetic Diversity, 'Establishment of high-efficiency SNP-based mapping tools and development of methods for genome-wide mutation detection' PIS: Thomas Altmann, Thomas Mitchell-Odds, Bernd Weisshaar!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:3702"
/clone lib="Arabidopsis thaliana (Gueckingen-0 accession)
genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              449 AAGAATCAGTGCATTAACCTTGAAGGAGCAAAACATGGATCTTGCAACTATGTCTTCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.6%; Score 122.6; DB 11; Length 602; 87.6%; Pred. No. 1.4e-26; Live 0; Mismatches 19; Indels 0;
                                                                                                                                                                                                                                                                      94 degrees for 2.00 minute(s) 94 degrees for 0.50 minute(s) 58 degrees for 0.50 minute(s) 72 degrees for 1.00 minute(s)
                                                                                                                                                                                                                                                                                                                                  Annealing: 58 degrees for 0.50 minut
Polymerization: 72 degrees for 1.00 minut
PCR Cycles: 35
Thermal Cycler: Perkin Elmer Geneamp9600
organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTCACAAGTGTATCTGTTACGTCCCATGTTAA 357
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Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Template: 20 - 100 ng
Primer: each 1 uM
dNTPs: each 400 uM
Tag Polymerase: 0.05 units/ul
Total Vol: 10 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic_DNA"
/strain="Gueckingen-0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AB017065.1 GI:3510341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.5 mM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KCl: 50 mM
Tris-HCl: 10 mM
pH: 8.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .602
                                                                                                                                                                                                                                                                                                     Denaturation:
                                                                                                                                                                                                                         STS size: 602
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                       Protocol:
Template:
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source

FEATURES

Best Local

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ORIGIN

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 12 AB017065/c LOCUS DEFINITION

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CDS

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join(34960. .35217,35310. .35423,35504. .35611,35705. .35796,35690. .36631,36106. .36200,36301. .36430,36509. .36653,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not experimental
/product="calmodulin-like protein"
/protein id="BAB09153.1"
/db xxef="d1.978699"
/translation="WEINNEKKLESRQSSFRIRSPSINALRIHRVPDLFDKGNUDGFI
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CCDGSPESDLERARNFOEDGGFISAVELQKVLKKLGLPEAGLHKTLDESFFGGEGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /evidence=not_experimental
/protein_id="BAB09154.1"
/bc.kref="G1:9789700"
/translation="MIEVTREAVEQAVIDTREWIENIATSEOGTSGSGLGWIIRNSHGT
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FMECGMSKRQGRAPVEESECTALIWALQSSWNLGYIKIEFDGDNLSIIRLINGKAVNP
                                                                                                                                                                                                                                                                         /translation="WWREEIGEGBETKKTQWYRDGVSYWEGVEASVDGVLGGYGHVND
ADLIGSBEWEKTLLOBRLWNGANGHLVALDGSGGIGRITKHLIRYKFRENEVDLEBV
AQFLDAARBYLAKAGSETHKATWFFVYPLOBFTPAAGRYDV WVQWCIGHLDNDFVS
FFNRAKDLFWIKRIIASPDRIHTSNSSFANGGYISIEGRNLQSFLONNFQDQKGLPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
protein_id="BhB09155.1"
/db_xref="GI:9758701"
/translation="MLNSGURTQRRSPRPLSLGGRKIITPTKFAYDHHNPDKVLDFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC004747 87080 bp DNA linear PLN 11-MAR-2002
Arabidopsis thaliana chromosome 2 clone T19L18 map B68, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMDCLEPKTKNNLTGKLLLVASLLILAIIVISQSSSFTSPSAFSQREEGVTHVLVTGG
                            complement(join[27805, .27967,28028, .28125,28368, .28469,
28564, .28674,28765, .28823,28902, .29049,29157, .29234))
/note="gene_id:MFC16.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="contains similarity to UDP-glucose 4-epimerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 61290;
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                                                                                                                                                                                                                                                                                                                                                                                                     ELFAVKMYALTVDTPPKIHRTRSKTRSNRPQIIK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(32184, .32265,32365, .32609)
Antes=361 AAR30348.1
gene id:MFC16.13
similar to unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.6%; Score 122.6; DB 8;
llarity 87.6%; Pred. No. 1.4e-26;
Conservative 0; Mismatches 19;
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                                                                                                                                                                                          experimental
                                                                                                                                                                                                                /protein_id="BAB09152.1"
/db_xref="GI:9758698"
                                                                                                                                                                                                                                                                                                                                                                                                                                 30731. .31276
/note="gene_id:MFC16.12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      id:MFC16.15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36862. .37088)
                                                                                                                                                                                       /evidence=not
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AC004747.3
HTG.
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Matches 134; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence.
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AC004747/c
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VERSION
KEYWORDS
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EMSWIESVLWFIKGESMEILAKRKRTSRSFKGKDDFIEEPIPKTALQYLWRRFEAPEA RLAKIILTPFGGKMSEIADNEIPFPHREGNLYEIQYLAYWSEBEDKNKTNTEKYLRWV SYVERWIPYVSKSPRRAYNBRDIDLGMYLGLNMKTKYEEAKVWGVKYFKNNFDRLV RVKTNVDPMPPFCDEQSIPIMKYYNDI.
join(7391. 7708,7913. .8716,8797. .8955,9026. .9446,9636. .9820)
/note="contains similarity to En/Spm-like transposon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MAKSATIITFLFAALVLFAAFEAPTMVEAQKLCEKPSGTWSGVC
GNSNACKNQCINLEGAKHGSCNYVFPAHKCICYVPC"
complement (24139. .25740)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPKVIHTSKDSSFPSILDSSIQNPRFSVSETPKPVSIITPVKASDVQTVIRCAQLHGI
HVRTRSAGHCYEGLSYIAYNKPFAVIDLRNLRSISLDVDNRTGWVQTGATAGELYYEI
GKTTKSLAFPAGIHPTVGVGGQFSGGGYGTLLRKYGLAADNIIDALVVDASGRILDRQ
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ARLGKIILTPFGGKMSEMAEYETPFPHRGGNLYEIQYVAYWREEEDKNKTETDKYLKW
VDSVYEFWTPYVSKSPRGAYVNFKDMDLGMYLGKKKTKYEEGKSWGVKYFKNNFERLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DVEEKLEEFKSEKSTARLKLAILLFLAKVWKADSKGDSKIEBFLLRIVDNVRACETFP
WGRFSFEQCMBGVQRVWKNKKGVVKQKAQTAFYGFITPLEILAFECIPQLGKRFREVV
RADKECPRWCKHKFSESCMKGFTLEEINBALGOITDLSSILEPDMDERKALSRVVEKH
VUDGIGYIDJVUSWRERLIVEKKKIEFRSLYQADIDGRRIETVUDVPAVPEPPEIPGT
SILSFKEAMBRGFDKLTDKLAVMDSEIKRICLRVQGIESTVADQLEKKABKOKEDMC
PGDGSDESDBEDKKKKKKRQISKKRKYUQPTLESGKKRGRKPSKYKGEEFTAEGKQT
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ADKVPDDLFIRTTLERSNKNAVHALFTGLYIGPVNNLLALMEEKFPELGLEKEGCEEM
                                                                                                                                                                                                                                                                                                                                                                                                  /tränslation="marvkdssgeyestrstrestgeippsvdetaaeipgrdeegaell
TTEEEAGEIQPTTGDCDAADLGNSNAVAWESIDDLSNPNADSCAEEEEATNAVVQHDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MAKFASIITLIFAALVLFAAFDAPAMVEAQKLCEKPSGTWSGVC"
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pir.|T10624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VDQMGFLGSEP"
                                                                                                                                                                                                                       complement
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I (bases I to 87080)

Rounsley, S.D., Kaul, S., Lin, X., Ketchum, K.A., Crosby, M.L., Brandon, R.C., Syxes, S.M., Mason, T.M., Kerlavage, A.R., Adams, M.D., Somerville, C.R. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                       Genomic Research, 9712
                                                                                                                                                                                                                                                                                                                                                                                                                                                  9712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="synonym: T19118.1; supported by cDNA:
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                                                                                                                                                                                                                                                                                                                                                                                            Town, C.D. and Kaul, S.
Direct Submission
Submitted (27-FEB-2002) The Institute for Genomic Research, 9
Medical Center Dr, Rockville, MD 20850, USA, cdrown@rigr.org
On Apr 18, 2002 this sequence version replaced gi:6598441.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .2572,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="gynonym: T19L18.3; predicted by genscan"
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Submitted (09-MAR-2000) The Institute for Ger
Medical Center Dr., Rockville, MD 20850, USA
3 (bases 1 to 87080)
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                                                                                                                                                                                                                               Unpublished
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     SOURCE
ORGANISM
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REFERENCE
AUTHORS
TITLE
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TITLE
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FEATURES
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QBSJALLLEVELIALSGEIPVMLTQNQSNLAYDPALEASSEIIDIPAQKETCN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(13028. .13137,13438. .13642,13658. .13791,
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                                     Arabidopsis thaliana (mare cless).

Arabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 580)

Schmid,K.J., Sorensen,T.R., Stracke,R., Torjek,O., Altmann,T.,
Mitchell-Olds,T. and Weisshaar,B.

Large-Scale Identification and Analysis of Genome-Wide

Single-Nucleotide Polymorphisms for Mapping in Arabidopsis thaliana

Genome Res. 13 (6), 1250-1257 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 degrees for 2.00 minute(s) 94 degrees for 0.50 minute(s) 58 degrees for 0.50 minute(s) 72 degrees for 1.00 minute(s) 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermal Cycler: Perkin Elmer Geneamp9600
                                                                                                                                                                                                                                                                                                                                                                                                      Winzerlaer Str. 10, 07745 Jena, Germany
Tel: + 49-3641-571465
Fax: + 49-3641-571462
Emal: schmid@ice.mpg.de
Primer A: CGCTGCTCTTGTTCTTTG
Primer B: AAACAAACCGTTGTTGGTCA
STS size: 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                 Synonyms: PCP16C2 cvi0.a
Contact: Karl Schmid
Department of Genetics and Evolution
Max-Planck Institute of Chemical Ecology
                          Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tag Polymerase: 0.05 units/ul Total Vol: 10 ul
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each 1 uM
each 400 uM
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Location/Qualifiers
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KC1: 50 mM
Trie-HC1: 10 mM
pH: 8.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymerization:
PCR Cycles:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Best Local Similarity
Matches 133; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Presoak:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer:
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                                            ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MASC_STS16438 Arabidopsis thaliana (Cap Verde Islands-0 accession)
genomic DNA Arabidopsis thaliana STS genomic, sequence tagged site.
BV010699.1 GI:32963197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /trānglation="MTNGGGGMSSGEGFRRRSSGEGFPAREFRWVSGDRVFPRGFFG
EGYQVGVFTVVSGEGVPAKVPGGDFSGKKVPAVVFRRVSSSDGGGRGSGGGGGGGGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /trānalation="MCFYLLSEKNQTHPSPSSSPFLSEQRTQPKQKSMLDMSESVLTAMYSWFTPTVLFVFLNLMIGTIAISSSFSKSNDPNQTQIQRSPSMIHRLKSINFSSFT
                       ISYVCRKKI QYDMEEBGTLYRADNIKHAGTPSPSKFSPYSLYFKGIMKGPIHDSAITL
LEAELMALKYGLSEAVTLGINHISICCDNNQIFEWYMGRSTPQEENIAMLIRDVQGIR
KQPTSSIAVLVTRNQVEFAYKVAMEAICFKTKIAFSVSSDVPALFHPKKTCTICFDDD
                                                                                INADMMFYIDQCGHMFCSECVKRHIEGSLITCPSYRCKSKLIYGSCVNILTPKVKEMM
IQRMGEDSIPYTDRYYCPNPTCSALMSVTELDQLTGNVDMSFAMDVELMLDVALMVMY
RIFQLNVSSQKSKH"
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PFCVKCKVSWHNNLSCDEYKTLHPNPTENDGRLRDLANEKSWRQCSKCKHMIELSSGC
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                                                                                                                                                                                                                                                                                                                                        /note="synonym: T19L18.7; predicted by genefinder"
complement(join(<20678. .20845,20919. .>21065))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 8; Length 87080;
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Pred. No. 1.3e-26;
0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           complement (join (20678. .20845, 20919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein"
/protein_id="AAC31225.1"
/db_xref="G1:3413702"
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complement(21861. 21943)
/rpt_family="AT_rich"
complement(22621. 23626)
/gene="At2g26110"
/note="Rynow;" T19118.8"
complement(<22621. >23626)
/gene="At2g26110"
                                                                                                                                                     complement (14765. .14967)
/rpt family="AT rich"
complement (18680. .18732)
/rpt family="AT_rich"
19418. .19445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="unknown protein"
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complement(21381. .21433)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="(TGG)n"
21200. .21221
/rpt_family="(A)n"
                                                                                                                                                                                                                                                                                                                                                                                     'gene="At2g26120"
                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="At2g26120"
codon start=1
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Matches 134; Conservative
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BV010699
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Search completed: May 18, 2004, 17:59:04 Job time: 758.05 secs
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Large-Scale Identification and Analysis of Genome-Wide
Single-Nucleotide Polymorphisms for Mapping in Arabidopsis thaliana
Genome Res. 13 (6), 1250-1257 (2003)
                                                                                                                                                                                                BV010698 STS16439 Arabidopsis thaliana (Konchezero accession) genomic DNA Ārabidopsis thaliana STS genomic, sequence tagged site.
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                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae, Arabidopsis.

1 (bases 1 to 582)
153 AAGAATCAGTGCATTAACCTTGAGGGAAGCAAAACATGGATCTTGCAACTATGTCTTCCCA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana (Konchezero accession)
genomic_DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 degrees for 2.00 minute(s) 94 degrees for 0.50 minute(s) 58 degrees for 0.50 minute(s) 72 degrees for 1.00 minute(s) 35
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PCR Cycles: 35
Thermal Cycler: Perkin Elmer Geneamp9600
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/mol_type="genomic DNA"
/strain="Konchezero"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synonyms: PCP16C2_cs22491.a
Contact: Karl Schmid
Department of Genetics and Evolution
Max-Planck-Institute of Chemical Ecology
Winzerlaer Str. 10, 07745 Jena, Germany
Tel: + 49-3641-571462
                                                GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                       213 GCTCACAAGTGTATCTGTTACGTCCCATGTTAA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.05 units/ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: schmid@ice.mpg.de
Primer A: CGCTGCTCTTGTTTG
Primer B: AAACAAACCGTTGTTGGTCA
STS size: 582
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 - 100 ng
each 1 uM
each 400 uM
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BV010698.1 GI:32963196
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MgCl2: 1.5 mM
KCl: 50 mM
Tris-HCl: 10 mM
PH:
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Total Vol: 10 ul
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Annealing:
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BV010698
LOCUS
DEFINITION
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AUTHORS
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94 AAGTIGIGGGAGAAGCCAAGIGGIACTIGGICAGGAGTITGCGGAAACAGCAATGCATGC
                                                                                                                                                                                                                                                                                                       62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA
                                                                                                                                                                                                 2 AGGITGIGCGAGAGACCAAGIGGGACAIGGICAGGAGTITGIGGGAACAACAAIGCAIGC
                                                                                                                                                  Gaps
                                                                                                                                                  0;
                                                                                                   Length 582;
                                                                                                Score 121, DB 11, Length 5 Pred. No. 4.3e-26, 0; Mismatches 20; Indels
Thomas Mitchell-Olds, Bernd Weisshaar"
<1. .>582
                                                                                                                                                                                                                                                                                                                                                                                                                                  214 GCTCACAAGTGTATCTGTTACGTCCCATGTTAA 246
                                                                                                                                                                                                                                                                                                                                                                                                     122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                   Query Match 78.6%;
Best Local Similarity 86.9%;
Matches 133; Conservative
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This sequence represents the cDNA sequence cloned into the E. coli cassette vector pMON23317 to generate vector pMON22652. The cDNA encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alyssum antifungal polypeptide and corresponding DNA - used in the production of transgenic plants resistant to phytopathogenic fungi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; Page 69; 92pp; English.
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P-PSDB; AAW35560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aat94582 Amplified
Aat94574 Alyssum s
Aat9289 Alyssum s
Aat94581 Composite
Adc51221 Brassica
Adc51223 Brassica
Adc68378 Arabidops
Aav10632 A. thalia
Abg6269 Wasabia j
Abz4241 Arabidops
Abz4241 Arabidops
Abz42136 Arabidops
Aav10633 A. thalia
Aag38650 Rs-AFP1 C
Aag38650 Rs-AFP1 C
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Aaz39123 Wasabia j
Abg28291 Wasabia j
Aaz39124 Wasabia j
Aav10646 A. thalia
Aat94577 Cloned 5'
Aag4577 Cloned 5'
Aag70130 Antimicro
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                                                                       May 18, 2004, 16:12:26; Search time 150.15 Seconds (without alignments) 4357.126 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                               1 aaggttgtgcgagagaccaa......tttgttacttcccatgttaa 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
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Aaq70128 A
Aat72333 R
Aat68696 R
Aaz39123 W
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                          3373863 seqs, 2124099041 residues
                                                                                                                      US-10-681-972-12_COPY_116_269
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Maximum Match 100%
Listing first 45 summaries
                                                 - nucleic search, using sw model
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AAT94581
AAT94289
AAT94289
ADC51221
ADC61223
ADAC6123
AAV10632
AAV10633
AAV38650
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AAZ39124
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L: geneseqn1980s:*
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Maximum DB s
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9 t	105	68.2	485	m (AAZ99333	Aaz99333	DNA
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45	45.2	29.4	577	m	AAZ51378	Aaz51378	Dahlia
					ALIGNMENTS		
RESULT 1							
AATS	582 AAT94582 st	standard;	I; DNA;	270	BP.		
AATS	AAT94582;						
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121	-MAY-1998) (Ilrst	rst entry)	<u> </u>			
Amplifi	eq	Alyssum	speci	es a	antifungal polypeptide ge	gene from pMO	pMON22652.
Anti	Antifungal polypeptide; phytopathogenic fungus;	polype yenic f		AlyAFP resist	AFP; inhibition; transgeni istance; ss.	enic plant;	
Alye	Alyssum sp.						
Key		нα	ocation	1/0n	alifiers		
sig	peptide	e,	/*tag= a /product= "AlyAFP 22108	ug II P	antifungal	polypeptide"	
mat	peptide	e •	/*tag= 10925 /*tag=	ပည္သ			
W097	WO9737024-A	- A 2 .					
0-60	-OCT-1997	7.					
27-N	-MAR-1997	7; 97	97WO-US00570	0570	. რ		
29-N	29-MAR-1996	•-	96US-00627706	2770	6.		
(MONS	~	MONSANTO	89				
Liand	J,	Shah D,	Wu Y,		Rosenberger CA;		
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the antifungal polypeptide AlyAFP, isolated from plants of the genus Alyssum. The AlystP polypeptide can be used to control phytopathogenic fungi, whilst the coding DNA can be used to produce transgenic plants that express the polypeptide making them resistant to the phytopathogenic
                                                                                                                                                                                                                                                61 CAGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCC 120
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                                                                                                                                                                                                                         9
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                                                                                                                                                                                      Gaps
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                                                                                                                                             Similarity 100.0%; Score 154; DB 2; Length 270; Similarity 100.0%; Pred. No. 1.9e-42; 54; Conservative 0; Mismatches 0; Indels 0
                                                                                                              Seguence 270 BP; 75 A; 58 C; 60 G; 75 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                        AGCICACAAAIGIATITGITACITCCCAIGITAA 154
                                                                                                                                                                                                                                                                                                                                                                                                228 AGCTCACAAATGTATTTGTTACTTCCCATGTTAA 261
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Matches 154;
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Antifungal polypeptide, AlyAFP; inhibition; transgenic plant; phytopathogenic fungus; resistance; ss. Alyssum species anti-fungal polypeptide AlyAFP cDNA sequence AAT94574 standard; cDNA; 286 (first entry) 12-MAY-1998 AAT94574;

RESULT 2 AAT94574

location/Qualifiers .17. .269 /*tag= a Alyssum

WO9737024-A2

"mature AlyAFP protein" start codon given at 5' end of sequence"

"no start

/product= /note= "no

09-0CT-1997

96US-00627706 29-MAR-1996;

97WO-US005709

27-MAR-1997;

(MONS) MONSANTO

Rosenberger CA; Wu Y, WPI; 1997-503109/46. Liang J, Shah D, P-PSDB; AAW35558

Claim 12; Page 68; 92pp; English.

Alyssum antifungal polypeptide and corresponding DNA - used in the production of transgenic plants resistant to phytopathogenic fungi

This sequence encodes the mature protein of an antifungal polypeptide (AlyARP) isolated from plants of the genus Alyssum. The sequence was PCR amplified using primers AAT94583-T94584, and the resultant 264 bp fragment was cloned as a BamHI fragment into the expression vector pMOM23317 to generate plasmid pMOM2552. The AlyARP sequence in this plasmid is placed under control of an B35S promoter and the maize HSP70 intron I sequence. The protein can be used to control phytopathogenic

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                                                                                                                                                                                 CAGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCC 120
                                                                                                                                                                                                          CAGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCC 235
fungi, whilst the DNA can be used to produce transgenic plants that express the protein making them resistant to the phytopathogenic fungi
                                                                                                                                                     116 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG
                                                                                                                           1 AAGGITGIGCGAGAGCCAAGIGGGACAIGGICAGGAGITIGIGGGAACAACAAIGCAIG
                                                                                               Gaps
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                                                                   Length 286;
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                                                                                               0; Indels
                                         Sequence 286 BP; 80 A; 62 C; 65 G; 79 T; 0 U; 0 Other;
                                                                    DB 2;
                                                                                                                                                                                                                                                        AGCTCACAAATGTATTTGTTACTTCCCATGTTAA 269
                                                                    100.0%; Score 154; DB 2;
100.0%; Pred. No. 2e-42;
ive 0; Mismatches (
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53. .292
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                                                                                  Similarity
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                                                                    Query Match
Best Local S
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Novel protein from Brassica campestris, useful as antimicrobial against plant pathogenic filamentous fungi or pathogenic bacteria, especially for treating e.g. rice white leaf blight and sheath blight disease.
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219 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACAGGGATCTTGCAACTATGTCTTCCCA 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention comprises the amino acid and coding sequences of antimicrobial (defensin) proteins from Brassica. The DNA and protein sequences of the invention are useful for producing transformed plants with composite disease resistance, especially resistant to diseases caused by pathogenic bacteria, such as: rice white leaf blight, brownstripe disease, glume blight, and seedling damping-off disease. As well as diseases caused by filamentous fungi, such as: rice blight, sheath blight disease, and leaf blight. The present DNA sequence encodes a Brassica defensin protein of the invention.
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/product= "Brassica oleracea defensin protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               composite disease resistance; pathogenic bacteria; rice white leaf blight, brown-stripe disease; glume blight; seedling damping-off disease; filamentous fungi; rice blight; sheath blight disease; leaf blight; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brassica oleracea defensin protein coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antimicrobial protein; defensin; transgenic plant;
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                                                                                     122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA
                                                                                                                     279 GCTCACAAATGTATTTGTTACTTCCCATGTTAA
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Matches 134; Conservative
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                                                                                                                                                                                                                                                          139 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG 198
                                                                                                                                                                                                                                                                                                                  CAGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCC 120
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                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Composite cDNA sequence for Alyssum species antifungal polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alyssum antifungal polypeptide and corresponding DNA - used in the production of transgenic plants resistant to phytopathogenic fungi
                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide making them resistant to the phytopathogenic fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91.0%; Score 140.2; DB 2; Length 500; llarity 94.8%; Pred. No. 1.3e-37; Conservative 0; Mismatches 8; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide; AlyAFP; inhibition; transgenic plant; genic fungus; resistance; ss.
                                                                                  Length 481;
                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 500 BP; 145 A; 89 C; 111 G; 154 T; 0 U; 1 Other;
                             Sequence 481 BP; 147 A; 88 C; 91 G; 154 T; 0 U; 1 Other;
                                                                                                                                                ..
0
                                                                                  100.0%; Score 154; DB 2; 100.0%; Pred. No. 2.4e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                  121 AGCTCACAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCTCACAAATGTATTTGTTACTTCCCATGTTAA
                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosenberger CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Page 67; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-US005709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT94581 standard; DNA; 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                             Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MONS ) MONSANTO CO.
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                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 145; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shah D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antifungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alyssum sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259
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                                                                                           Query Match
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211 GCTCACAAGTGTATTTGCTACTTCCCTTGTTAA 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
AAV10632
ID AAV10632 standard; DNA; 403
                                                                                                             ADA68378 standard; DNA; 243
                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            illustrate the invention.
                                                                                                                                                                                                                                                                                          Arabidopsis thaliana,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quan S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-175290/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W,
                                                                                                                                                                                                                                                                                                                              WO2003000898-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chang H, Ch
Katagiri F,
                                                                                                                                                                                   20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                  03-JAN-2003
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                                                                                                                                                 ADA68378;
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                                                                                            ADA68378
                                                                       RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel protein from Brassica campestris, useful as antimicrobial against plant pathogenic filamentous fungi or pathogenic bacteria, especially for treating e.g. rice white leaf blight and sheath blight disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 AAGTTGTGCGAGAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention comprises the amino acid and coding sequences of antimicrobial (defensin) proteins from Brassica. The DNA and protein sequences of the invention are useful for producing transformed plants with composite disease resistance, especially resistant to diseases caused by pathogenic bacteria, such as: rice white leaf blight, brownstripe disease, glume blight, and seedling damping-off disease. As well as diseases caused by filamentous fungi, such as: rice blight, sheath blight disease, and leaf blight. The present DNA sequence encodes a Brassica defensin protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                     antimicrobial protein; defensin; transgenic plant; composite disease resistance; pathogenic bacteria; rice white leaf blight; brown-stripe disease; glume blight; seedling damping-off disease; filamentous fungi; rice blight; sheath blight disease; leaf blight; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 79.6%; Score 122.6; DB 9; Length 426; Best Local Similarity 87.6%; Pred. No. 1.3e-31; Matches 134; Conservative 0; Mismatches 19; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 426 BP; 142 A; 72 C; 84 G; 128 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/product= "Brassica defensin protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH
                    122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                               211 GCTCACAAGTGTATTTGCTACTTCCCTTGTTAA
                                                                                                                                                                                                                                                       Brassica defensin protein coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; SEQ ID NO 3; 34pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                      location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-SEP-2001; 2001JP-00283117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-SEP-2001; 2001JP-00283117
                                                                                                                                               ADC51223 standard; DNA; 426
                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-621123/59.
P-PSDB; ADC51224.
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                                                                                                                                                                                                                   18-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                  Brassica sp
                                                                                                                                                                               ADC51223;
                                                                                                                            ADC51223
                                                                                                           RESULT
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The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 AAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AGGITGIGGGAGAGCAAGIGGGACAIGGICAGGAGITIGIGGGAACAACAAIGCAIGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTTCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                              Plant; bacterial infection; fungal infection; viral infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zon ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 7; Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goff SA, Ho
e Z, Zhu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 77.5%; Score 119.4; DB 7; Length Best Local Similarity 86.3%; Pred. No. 1.3e-30; Matches 132; Conservative 0; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 243 BP; 58 A; 56 C; 59 G; 70 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glazebrook J, Goff
Whitham S, Xie Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTCACAATGTATCTGCTACTTCCCATGTTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; SEQ ID NO 747; 899pp; English.
Arabidopsis thaliana gene, SEQ ID 747.
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P-PSDB; ABP53725
                                                                                         Eutrema wasabi,
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                           02-JAN-2003
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                                                                                                                                                                       24-SEP-2002
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                                                                                                                                                                                                                                                                                                                                            Protecting plants against pathogens by inducing defensin genes - by stimulating ethylene or jasmonate pathways, also new promoter of defensin gene from Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
                                                                                                                                                                                                                                                                                                                                                                                               This sequence encodes the Arabidopsis PDF1.1 gene which is used in a novel method for the protection of plants against pathogens which involves inducing expression of a plant defensin gene by stimulating the jasmonate and/or ethylene pathways. The method is used to induce protection against necrotrophic pathogens, specifically fungi and does not require cytotoxic or potentially harmful chemicals
                                                                                                                                                                                                                                                                                         Manners JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                            Defensin; PDF1.1; protection; plant; pathogen; jasmonate; ethylene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.5%; Score 119.4; DB 2; Length 403; 86.3%; Pred. No. 1.5e-30;
                                                                                                                                                                                                                                                                                         Terras FRG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 403 BP; 112 A; 77 C; 85 G; 129 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 GCTCACAAATGTATCTGCTACTTCCCATGTTAA 268
                                                                                                                                                                                                                                                                                       Thomma BPHJ, Penninckx IAMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                              'note= "plant defensin"
                                                                                                        Location/Qualifiers
                                                                                                                                                                      "PDFI.1"
                                                                                                                                                                                                                                                                                                                                                                                Disclosure, Fig 1, 72pp, English.
                                                                                                                                                                                                                                    97WO-GB001672.
                                                                                                                                                                                                                                                     96GB-00013753
                                                                                                                 26. .268
/*tag= a
26. .113
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/product=
                         (first entry)
                                                                                                                                                    .265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 86.3
hes 132; Conservative
                                                                                                                                            *tag=
                                           A. thaliana PDF1.1 DNA
                                                                                      Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                  WPI; 1998-086663/08.
                                                                                                                                                                                                                                                                                                                            P-PSDB; AAW40345.
                                                                                                                                                                                                                                                                      (ZENE ) ZENECA
                                                                                                                                                                                                                                                                                       Broekaert WF,
                                                                                                                                                                                                WO9800023-A2
                                                                                                                                                                                                                                    20-JUN-1997;
                                                                                                                                                                                                                                                     01-JUL-1996;
                         23-JUN-1998
                                                                                                                                   sig_peptide
                                                                                                                                                    mat_peptide
                                                                                                                                                                                                                  08-JAN-1998
                                                                      fungi; ss
        AAV10632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                  Kazan K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
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원
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ABQ82690 standard; cDNA; 243 BP

ABQ82690 ID ABO8

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                 Wasabia japonica; gamma-thionin; plant; disease-resistant plant; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 AAGAATCAGTGCATCAACCTTGAGGGAGCACGACATGGATCTTGCAACTATATCTTCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 AAGTTGTGCGAGAAGTCAAGTGGAGAACATGGTCAGGAGTCTGTGGAAACAACAATGCGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a disease-resistant plant in which wasabi gamma-thionin gene is introduced. Also described is a method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A disease-resistant plant in which wasabi gamma-thionin gene introduced, creation of the disease-resistant plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana stress regulated gene SEQ ID NO 2046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
                                                   Wasabia japonica gamma-thionin encoding cDNA SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 243 BP; 60 A; 54 C; 55 G; 74 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 76.5%; Score 117.8; DB 6; Best Local Similarity 85.6%; Pred. No. 4.4e-30; Matches 131; Conservative 0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211 TATCACAGATGTATCTGTTACTTCCCATGTTAA 243
                                                                                                                                                                                                                                                                                   /*tag= a
/product= "gamma-thionin"
                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 8; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAR-2001; 2001JP-00083526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-MAR-2001; 2001JP-00083526.
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(first entry)
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Zhu T;

Wang X,

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cell has been exposed, comprising: (a) contacting nucleic acid arrepresentative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants. Cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to berwent by the European Patent Office
                                                                                                                                                                                                                                                                                                          Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
                                                                                                                                                                                                                                                                                                                                                                                          invention relates to identifying a stress condition to which a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Posttranscriptional gene silencing; PTGS; plant; transformation; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AGGITGIGCGAGAGACCAAGIGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATGC
                                                                                                                                                                                                                                                                                                                                                            Claim 144; SEQ ID NO 2046; 577pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 243 BP; 62 A; 57 C; 58 G; 66 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana gene #120 modulated by PTGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTCACAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SCRI ) SCRIPPS RES INST.
(SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                             24-AUG-2000; 2000US-0227866P.
26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
                                                                                            24-AUG-2001; 2001WO-US026685.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 76.5%;
Best Local Similarity 85.6%;
Matches 131; Conservative
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                                                                                                                                                                                                                                              Kreps J,
Arabidopsis thaliana
                                                                                                                                                                                                                                                                              WPI; 2002-304127/34
                              WO200216655-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-FEB-2003
                                                               28-FEB-2002
                                                                                                                                                                                                                                                Harper JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
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ABZ42136
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Score 117.8; DB 6; Length 243; Pred. No. 4.4e-30; 0; Mismatches 22; Indels 0;

Location/Qualifiers 1. .243

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The invention relates to a novel isolated polynucleic acid segment modulated within a cell by posttranscriptional gene silencing (PTGS). The invention specifically relates to a method to identify an expression product that is modulated by PTGS. The polynucleotide is useful for modulating the gene expression within a cell by PTGS, by introducing the polynucleic acid into a cell and expressing the nucleic acid segment in the cell to form a product. The polynucleic acid segment is also useful for augmenting a cell and expressing the nucleic acid segment in contacting a plant cell with the segment to produce a transformed plant cell, and growing the transformed plant to produce a transformed plant segments of A. thaliana cDNA modulated by PTGS
                                                                                                                                                                                                                                                               Novel polynucleic acid segment useful for modulating gene expression within a cell by posttranscriptional gene silencing, and for augmenting plant cell genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 AAGAATCAGTGCATTAACCTTGAAGGAGCCAAACATGGATCATGCAACTATGTCTTCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGAACCAATGCAGAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Defensin, PDF1.2; protection, plant, pathogen, jasmonate; ethylene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 7; Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 117.8; DB 7; Length
Pred. No. 4.4e-30;
0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 243 BP; 62 A; 57 C; 58 G; 66 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCACACAAAGTGTATCTGTTACGTCCCATGTTAA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                           Chang 3
                                                                                                                                                                                                                                                                                                                                Claim 18; Page 425-426; 438pp; English.
                                                                                                                                                                                               Wang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 32. .274
                                                                                                                                                 (SYGN ) SYNGENTA PARTICIPATIONS AG. (FRIE-) FRIEDRICH MIESCHER INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                               Glazov EA, Meins F,
                                                                                                                   06-APR-2001; 2001US-0282049P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 85.6%;
Matches 131; Conservative
                                                                                     05-APR-2002; 2002WO-EP003806
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/*tag=
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                                                                                                                                                                                                                           WPI; 2003-103337/09.
                                                                                                                                                                                                                                         P-PSDB; ABP81292
                            WO200281695-A2.
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                                                        17-0CT-2002,
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                                                                                                                                                                                           Zhu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
AAV10633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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32. .119 /*tag= b 120. .271 *tag=

> sig_peptide mat_peptide

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This cDNA represents the sequence of Rs-AFP1 from Raphanus sativus. PCR primer AAQ38640 was used together with AAQ38641 to generate a probe for screening a Raphanus sativus seed cDNA library. This primer corresponds to amino acids 2 to 7 of Rs-AFP1 and has a sense orientation. The 144bp product, which was further reamplified with the same primers and digoxiganin-11-dUTP instead of dTTP to give a digoxiganin-11-dUTP instead of dTTP to give a digoxiganin-11-dUTP instead of dTTP to give a digoxiganin labeled PCR product. This was used to screen a lambda ZAPII CDNA library by in situ product. This was used to screen a lambda EAPII cDNA library by in situ additional screening rounds with the same probe. Inserts by in situ vivo into the pBluescript phagemid form with the aid of helper phage R408.Inserts from 22 positive clones were excised by BcoRI digestion and their size compared by agarose gel electrophoresis. Four clones had insert sizes of approx. 400bp the others between 250-300bp. The inserts compared their squeen defined and found to differ only in the length of their 5' and 3' UTR's. The longest sequence is given here. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of plants - e.g. brassica or resistance to fungal and bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 Aagaarcagigcarraaccirgagaaagcacgacarggarcrigcaacraigricriccca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 AGGITGIGCGAGAGACCAAGIGGGACAIGGICAGGAGITITGIGGGAACAACAAIGCAIGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 AAGTTGTGCGAAAGGCCAAGTGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 414;
                                                                                                                                                                                                                                                                                                                                                                                    Terras FRG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                    Rees SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.5%; Score 117.8; DB 2
85.6%; Pred. No. 5.5e-30;
iive 0; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
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                                                                                                                                                                                                                                                                                                                                                                                    Cammue BPA, Osborn RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biocidal proteins isolated from seeds dahlia, useful for increasing plants'
Location/Qualifiers
16. .256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 21; Fig 35; 110pp; English
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92GB-00013526.
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                                                                                                                                                                                            92WO-GB001570.
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(first entry)
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Matches 131; Conservative
                                            /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                            Vanderleyden J;
                                                                                                                                                                                                                                                                                                                                                                                    Broekaert WF,
                                                                                                                                                                                                                                      29-AUG-1991;
13-FEB-1992;
25-JUN-1992;
                                                                                                                                                                                            27-AUG-1992;
                                                                                              WO9305153-A1
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14-FEB-1995
                                                                                                                                             L8-MAR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protecting plants against pathogens by inducing defensin genes - by stimulating ethylene or jasmonate pathways, also new promoter of defensin gene from Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 AAGTIGIGGAGAAGCCAAGIGGGACAIGGICAGGGTIIIGCGGAAACAGIAAIGCAIGC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence encodes the Arabidopsis PDF1.2 gene which is used in a novel method for the protection of plants against pathogens which involves inducing expression of a plant defensin gene by stimulating the jasmonate and/or ethylene pathways. The method is used to induce protection against necrotrophic pathogens, specifically fungi and does not require cytotoxic or potentially harmful chemicals
                                                                                                                                                                                                                                                                                                                                                                                                                                Penninckx IAMA, Terras FRG, Manners JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGITGIGCGAGACCAAGIGGGACAIGGICAGGAGITTGIGGGAACAACAAIGCAIGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

76.5%; Score 117.8; DB 2; Length
Best Local Similarity 85.6%; Pred. No. 5.4e-30;
Matches 131; Conservative 0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 400 BP; 109 A; 82 C; 80 G; 125 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCACACAAGTGTATCTGTTACGTCCCATGTTAA 274
                                                                                              /*tag= c
/product= "PDF1.2"
/note= "plant defensin"
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Disclosure; Fig 1; 72pp; English.

97WO-GB001672. 96GB-00013753

20-JUN-1997; 01-JUL-1996;

WO9800023-A2

sroekaert WF, Thomma BPHJ,

Kazan K;

ZENE) ZENECA LTD.

WPI; 1998-086663/08.

P-PSDB; AAW40346

225

AAQ38650 standard; DNA; 414

RESULT 13 AAQ38650

242

62

qq

AAQ38650;

(first entry)

RS-AFP1 CDNA 25-MAR-2003 07-JUL-1993

Raphanus sativus

(revised)

Gaps

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(pos:85. .87, aa:Glu)

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                          symbiosis; disease-resistance; fungus-resistance; cynodontis; Cxc; crop improvement; endophyte; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antifungal protein; candida; fungal resistance; food additive; radish; crop protection; plant defensin; bacterial protection; preservative; ss.
                                                                                                                                                                                                                                                                                                                                                                                              Plant-derived antimicrobial proteins are expressed in endosymbiotic Clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with recombinant Cxc are protected against fungal disease. A suitable antimicrobial protein is Rs-AFP1 from R. sativus. The full-length cDNA sequence of Rs-AFP1 is given in AAQ70128. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                             Antimicrobial protein producing endo-symbiotic microorganisms - is produced by combining nucleic acids encoding the protein with an endophyte, useful for protecting plant hosts from esp. fungal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 117.8; DB 2; Length 414; Pred. No. 5.5e-30; 0; Mismatches 22; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Raphanus sativus antifungal protein I (Rs-AFP1) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTCACAAAIGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTCACAAGTGTATCTGCTACTTTCCTTGTTAA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
16. .258
                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 31; 39pp; English
                                                                                                                                                                                                                                           SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.5%;
85.6%;
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                                                                                                                                                                                  93GB-00000281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 131; Conservative
                         Antimicrobial, Rs-AFP1;
Clavibacter xyli subsp.
                                                                                                                                                                                                                                        Powell KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
Antimicrobial Rs-AFP1
                                                                                                                                                                                                                                                                      WPI; 1994-249223/30.
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Best Local Similarity
                                                                                                                                                                                                               (ZENE ) ZENECA LTD
                                                                                                                                                                                                                                                                                  P-PSDB; AAR57325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Raphanus sativus.
                                                                    Raphanus sativus
                                                                                                                                                                                  38-JAN-1993;
                                                                                                                                                       05-JAN-1994;
                                                                                               WO9416076-A1
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19-JAN-1998
                                                                                                                                                                                                                                           Dubock AC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This cDNA sequence encodes an Rhapanus sativus (radish) antifungal protein (Rs-AFP1). Analogues of the homologous protein, Rs-AFP2 (AAM19281), have also been produced (see AAM1928292, AAM19284-98, AAM19301-04, AAM19310-34 and AAM17165-834). Plants containing DNA sequences encoding these proteins have improved resistance to fungi. Compositions containing the peptides can be used to control fungi or bacteria in pharmaceutical (e.g. treatment of Candida infections) or preservative purposes (as food additives). In agriculture, the peptide may be used to improve disease resistance or disease tolerance of crops, either pre or post harvest. When applied to plants they may also have curative as well as protective actions. The peptides may also be used to protect plants by introducing them, or a microorganism capable of protect plants by introducing them, or a microorganism capable of the preservation of the soil. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 AAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGGATCTTGCAACTATGTCTTTCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 AGGITGIGCGAGAGACCAAGIGGGACAIGGICAGGAGITTGIGGGAACAACAAIGCATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 AAGTIGIGGGAAAGGCCCAAGIGGGACAIGGICAGGAGICIGIGGAAACAAIAACGCAIGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                       Sijtsma L, Van Amerongen A;
Borremans FAM, Rees SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Antifungal peptide derived from radish antifungal protein 2 - and DNA, useful for producing plants with increased fungal resistance therapeutic or preservative agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.5%; Score 117.8; DB 2; Length 414; ilarity 85.6%; Pred. No. 5.5e-30; Conservative 0; Mismatches 22; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
                                                                                      "antifungal_protein_1"
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                                                                                                                                                                                                                                                                                                                      Puijk WC, Schaaper WMM,
, Samblanx GW, Fant F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; Fig 2; 65pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 131; Conserv
                                                                                                                                                                                                                                                                                  (ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                                                                                    Meloen RH, Puij
Broekaert W, Sar
Van Gelder WMJ;
                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAW19280
                                                                                                                                                                                                                               13-DEC-1995;
28-MAR-1996;
                                                                                                                                                                                           12-DEC-1996;
                                                                                                                        WO9721815-A2
               sig_peptide
                                                                                                                                                          19-JUN-1997
                                                  mat_peptide
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Search completed: May 18, 2004, 17:22:40 Job time: 151.15 secs

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1 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGGAACAATGCATG
US-09-103-489-17
US-09-829-381D-17
US-08-377-192-50
US-08-777-192-50
US-08-377-687-31
US-08-377-687-31
US-08-377-687-31
US-08-377-687-33
US-08-777-192-31
US-08-777-192-31
US-08-971-982-31
US-08-971-982-31
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US-08-971-982-34
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US-08-971-982-36
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: COhen, Charles E.
REGISTRATION NUMBER: 34,5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 700 Chest
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
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Sequence 48, 1
Sequence 48, 1
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Sequence 12,
Sequence 12,
Sequence 12,
                                                                                                                                                                                                                                                                                                                                                                                                    154
1 aaggttgtgcgagagaccaa......tttgttacttcccatgttaa 154
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.: /cgn2 6/ptodata2/ina/5A_COMB.seq:*
.: /cgn2 6/ptodata2/ina/5B_COMB.seq:*
.: /cgn2 6/ptodata2/ina/6A_COMB.seq:*
.: /cgn2 6/ptodata2/ina/6B_COMB.seq:*
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.: /cgn2 6/ptodata2/ina/PCTUS COMB.seq:*
.: /cgn2 6/ptodata/2/ina/backfiles1.seq:*
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(c) 1993 - 2004 Compugen Ltd.
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US-09-103-489-9

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US-08-377-687-48

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US-08-777-192-48

US-08-777-192-8

US-09-077-948A-45

US-09-077-948A-45

US-09-077-948A-45

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US-09-077-958-58

US-09-0829-381D-5

US-08-977-192-58

US-08-971-982-58

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US-08-627-706-8

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US-09-103-489-16
US-09-829-381D-16
US-08-627-706-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                682709 seqs, 277475446 residues
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Maximum Match 1008
Listing first 45 summaries
                                                                                                                                                                          - nucleic search, using sw model
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seq length: 200000000
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                                                                                                                                                                                                                                             Run on:
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Best Local Similarity 100.0%; Pred. No. 2.8e-42;
Matches 154; Conservative 0; Mismatches 0; Indels
APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Ro. Dilip M.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 5773696th
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/627,706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE DOCKET NUMBER: 34,565
REFERENCE DOCKET NUMBER: 38-21(10700) A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314,537-6024
TELEPEAX: (314,537-6047
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 base pairs
TYPE: nucleic acid
STRANDEDMESS: single
TOPOLOGY: linear
MOLECULE TYPE:
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APPLICANT: Shab, Dilip M.
APPLICANT: Shab, Dilip M.
APPLICANT: Shab, Dilip M.
APPLICANT: Shab, Dilip M.
APPLICANT: Shab, Dilip M.
APPLICANT: Woming M.
TILLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control TILLE OF INVENTION: Plant Pathogenic Fungi
FILE REFERENCE: 38-J1 (10700) C
CURRENT APPLICATION NUMBER: US/09/829,381D
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR FILING DAIE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 14
LENGTH: 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 AAGGTTGTGCGAGAGCCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CAGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTTTCCC
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Patent No. 5773696

GENERAL INFORMATION:

APPLICANT: Liang, Jihong

APPLICANT: Shah, Dilip M.

APPLICANT: Shah, Dilip M.

APPLICANT: No. Yonnie S.

APPLICANT: Rosenberger, Cindy A.

TITLE OF INVENTION: Controlling Plant Pathogenic Pungi

TITLE OF INVENTION: Controlling Plant Pathogenic Pungi

TUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F

STREET: 70 Chesterfield Village Parkway No. 5773696th

CITY: St. Louis

STATE: Missouri

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 154; DB 4; Length 2; Pred. No. 2.8e-42; 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
AUPLICATION DATA:
RILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 AGCTCACAAATGTATTTTGTTACTTCCCATGTTAA 154
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                                   Sequence 14, Application US/09829381D Patent No. 6653280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Chen, Charles 34,565
REGISTRATION NUMBER: 34,565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

Best Local Similarity 100.0%;
Matches 154; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTHER INFORMATION: Plasmid US-09-829-381D-14
                                                                                                               GENERAL INFORMATION:
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108 AAGGTTGTGCGAGAGCCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG 167
                                                                           CAGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCC
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Sequence 14, Application US/09103489
Patent No. 6215048
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESS ADDRESS ADDRESS:
ADDRESS ADDRESS ADDRESS:
ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDRESS ADDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 6215048th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-UN-1998
CLASSIFICATION: 800
ATTORNEY/ABENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 34,565
TELEPHONE: (314) 537-624
TELEPHONE: (314) 537-624
TELEFRAN: (314) 537-6047
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 154; DB 3; Best Local Similarity 100.0%; Pred. No. 2.8e-42; Matches 154; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                          121 AGCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
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LENGTH: 270 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: CDNA
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RESULT 6
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US-08-627-706-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/09103489

Patent No. 6215048

GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 6215048th
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                                                                                                                                                                                                                                                                                    100.0%; Score 154; DB 1; Length 286; 100.0%; Pred. No. 2.9e-42; tive 0; Mismatches 0; Indels (
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-UN-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: COhen, Charles E.
REGISTRATION NUMBER: 34.565
REFERENCE/DOCKET NUMBER: 34.565
REFERENCE/DOCKET NUMBER: 34.565
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 AGCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 AGCTCACAAATGTATTTGTTACTTCCCATGTTAA 269
      38-21 (10700) A
REFERENCE/DOCKET NUMBER: 38-2
TELECPHONE: (314)537-6224
TELEPHONE: (314)537-6224
TELEPAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (314) 537-6224
TELEPAX: (314) 537-647
INPERATION FOR SEO ID NO: 12
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 286 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 63198
                                                                                                                                                                                                                                                                                    Query Match
Best Local Simi
Matches 154;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-09-103-489-12
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APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
APPLICANT: Shah, Jilip M.
APPLICANT: Shah, Jilip M.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control
TITLE OF INVENTION: Plant Pathogenic Fungi
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/09/829,381D
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR PILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 286
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                                                                                                                                                        61 CAGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCC
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                                                         0
        Length 286;
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Patent No. 5773696

APPLICANT: Liang, Jihong

APPLICANT: Shah, Dilip M.

APPLICANT: Wu, Yonnie S.

APPLICANT: Rosenberger, Cindy A.

TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
Query Match
100.0%; Score 154; DB 3;
Best Local Similarity 100.0%; Pred. No. 2.9e-42;
Matches 154; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 154; DB 4; 100.0%; Pred. No. 2.9e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Synthetic PCR reaction product
                                                                                                         1 AAGGITGTGCGAGAGCCAAGTGGGACATGGTCAGGAG
                                                                                                                                                                                                                                                                                                                                             236 AGCTCACAAAIGIAFITTGTTACTTCCCATGTTAA 269
                                                                                                                                                                                                                                                                                                                121 AGCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/09829381D Patent No. 6653280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 154; Conservative
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159 AAGTIGIGCGAGAGTCCAAGIGGAACAIGGICAGGCGIGIGIGGGGAAIAAIAACGCAIGC 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         279 GCTCACAATGTATTTGTTACTTCCCATGTTAA 311
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-UN-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles B.
REGISTRATION NUMBER: 34.565
REPERENCE/DOCKET NUMBER: 38-21 (1070
TELECOMMUNICATION INFORMATION:
TELEFNORE: (314) 537-624
TELEFXX: (314) 537-624
TELEFXX: (314) 537-624
TELEFXX: (314) 537-624
TELEFXX: (314) 537-624
TELEFXX: (314) 537-625
TELEFXX: (314) 537-627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       = any nucleotide
                                                                                                                                                                                                                                                                                                                                   LENGTH: 500 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature;
LOCATION: (22)...(22);
CTHER INFORMATION: N = US-09-829-381D-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Alyssum spp
                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: CDNA
US-09-103-489-9
                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
US-09-829-381D-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 AGGITGIGCGAGAGACCAAGIGGGACAIGGICAGGAGITIGIGGGAACAAIGCAIGC
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Charles E. Cohen, Monsanto Company, BB4F 700 Chesterfield Village Parkway No. 6215048th
          CORRESPONDENCE ADDRESS:
ADDRESSE: Charles E. Cohen, Monsanto Company, BB4F
STREET: TO Chesterfield Village Parkway No. 5773696th
CITY: St. Louis
CITY: Missouri
COUNTRY: USA
ZIP: 63198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: When, Dilip M.
APPLICANT: Womie S.
APPLICANT: Womenerger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEDE: Charles E. Cohen, Monsanto Company, BB4F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CAPRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
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                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 34,565
TELECOMMUNICATION INFORMATION:
TELEPRONE: (314,537-624
TELEPRONE: (314,537-6047
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/09103489
Patent No. 6215048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               500 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 700 Chest
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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Sequence 9, Application US/09829381D

| Sequence 9, Application US/09829381D
| Patent No. 6653280
| GENERAL INFORMATION:
| APPLICANT: Liang, Jihong
| APPLICANT: Rosenberger, Cindy A.
| APPLICANT: Rosenberger, Cindy A.
| APPLICANT: Rosenberger, Cindy A.
| TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control
| TITLE OF INVENTION: Plant Pathogenic Fungi
| FILE REFERENCE: 38 -21 (10700) C
| CURRENT APPLICATION NUMBER: US/09/829,381D
| PRIOR PILIATION NUMBER: 09/103,489
| PRIOR FILIATION NUMBER: 09/103,489
| PRIOR FILING DATE: 1998-06-24
| NUMBER OF SEQ ID NOS: 20
| SOFTWARE: PatentIn version 3.1
| LENGTH: 500
                                                                                                                                                                                                   219 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAAACACGGATCTTGCAACTATGTCTTCCCA 278
                                                                                                                                                                                                                                                                        62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
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                                                                                                                                      2 AGGITGIGCGAGAGCCAAGTGGGACATGGTCAGGAGITTGTGGGAACAACAATGCATGC
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DB 3; Length 500;
                                                                 Indels
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62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRICKATION:
PRICKATION:
PRICKATION DATA:
PRICKA APPLICATION UNMERR: US 08/002,480
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAMME: KOKULIS, PAUL N.
REGISTERATION NUMBER: 99042/SEE.36525/US/A
TELEPHONIS. 202-861-3000
TELEPHONE: 202-861-3000
TELEPHONE: 202-861-3000
TELEPHONE: 202-861-3000
TELEPHONE: 402-0944
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20005

MEDIUM TYPE: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,192
226 GCTCACAAGTGTATCTGCTACTTTCCTTGTTAA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
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         RESULT 11
US-08-777-192-48

Sequence 48, Application US/08777192

Patent No. 5824869

MENERAL INFORMATION:
APPLICANT: CAMMUE, BRUNO P. A.
APPLICANT: CAMMUE, BRUNO P. A.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESSE:
STREET.
                                                                                                                                                                                                                                                                                                                                                             STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
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US-08-777-192-48
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                                  219 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 AAGAATCAGTGCATTAACCTTGAGAAAGCACGAGGATCTTGCAACTATGTCTTCCCA 225
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  AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:

CLASSIFICATION: 800
PRIOR APPLICATION 1800
PRIOR APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISCHATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELEPHONIS, 202-861-3000
TELEPHAN: 202-861-3000
TELEPHAN: 202-861-3000
TELEPHAN: 202-81-3000
TELEPHAN: 414 hage PAIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,687
                                                                                     GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                              279 GCTCACAATGTATTTGTTACTTCCCATGTTAA 311
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                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: CESS, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSE: CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON
                                                                                                                                                                                            RESULT 10
US-08-377-687-48
; Sequence 48, Application US/08377687
; Patent No. 5538525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
16..255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA
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US-09-077-948A-45
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
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                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/971,982

PRIOR APPLICATION NUMBER: US 08/971,982

PRIOR APPLICATION NUMBER: US 08/02,480

FILING DATE: 04-JAN-193

ATTORNEY/AGENT INFORMATION:

NAME: KOKUJIS, PAUL N.

REGISTRATION NUMBER: 16,773

REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A

TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 GCTCACAGTGTATCTGCTACTTTCCTTGTTAA 258
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                                                                                                                                      REES, SARAH B.
THERAS, FRANKY R.G.
VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 48:
                                                                         APPLICANT: BROEKAERT, WILLEM F. CAMMUE, BRUNO P.A. OSBORN, RUPERT W.
               Sequence 48, Application US/08971982 Patent No. 6187904 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGHT, 414 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
16..255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                 STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE
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US-08-971-982-48
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RESULT 13
US-09-077-951-19
Sequence 19, Application US/09077951
Patent No. 6372888
GENERAL INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 76.5%; Score 117.8; DB 4; Length Best Local Similarity 85.6%; Pred. No. 4.2e-30; Matches 131; Conservative 0; Mismatches 22; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 GCTCACAAGTGTATCTGCTACTTTCCTTGTTAA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
APPLICANT: Brockaert, Willem
APPLICANT: Rees, Sarah
TITLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: PED50093
CURRENT FILING DATE: 1999-03-1.1
CURRENT PILING DATE: 1999-13-1.1
EARLIER APPLICATION NUMBER: GB 9525474.4
EARLIER PILING DATE: 1995-12-13
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PATENTING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PATENTING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PATENTING DATE: 1996-12-12
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PRIOR FILING DATE: 1996-12-12
PRIOR APPLICATION NUMBER: PCT/GB96/03068
PRIOR APPLICATION NUMBER: GB 9606552.9
PRIOR PLING DATE: 1996-03-28
PRIOR FILING DATE: 1995-12-13
NUMBER OF SEQ ID NOS: 141
SEQ ID NO 45
LENGTH: 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TILE OF INVENTION: Antifungal Proteins
PLE REPRENCE: 108946-257 (SYN-035)
CURRENT APPLICATION NUMBER: US/09/077,948A
CURRENT FILING DATE: 1998-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 45, Application US/09077948A
Patent No. 6605698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fant, Franky
Borremans, Frans
De Samblanx, Genoveva
Sitjtsma, Lolke
Meloen, Robbert
Puijk, Wouter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schaaper, Wilhelmus
Broekaert, Willem
Van Gelder, Wilhelmus
Rees, Sarah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Van Amerongen, Aart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Raphanus sativus
US-09-077-948A-45
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA; CRGANISM: Raphanus sativus US-09-077-951-19
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completed: May 18, 2004, 19:02:19

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 AAGAATCAGTGCATTAACCTTGAAGGAGCNCGACATGGATCTTGCAACTATGTCTTCCCA 278
                               166 AAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 AAGTIGIGGGAGAGTCCAAGTGGAACATGGTCAGGCGTGTGTGGAAACAACAATGCTTGC 218
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62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Way Yonnie S.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS: CORRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 5773696th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 63198
ZIP: 63198
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
                                                                                                                                                                                                              226 GCTCACAAGTGTATCTGCTACTTTCCTTGTTAA 258
                                                                                                                                                                                   122 GCTCACAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION ...
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21(10700)A
TELEPHONE: (314)537-6047
TELEPHONE: (314)537-6047
; INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
; SEQUENCE CHARACTERISTICS:
; SEQUENCE CHARACTERISTICS:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
STRAMUEDNESS: single
; TYPE: linear
; TOPOLOGY: linear
; TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08627706
Patent No. 5773696
GENERAL INFORMATION:
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Best Local Similarity 85.3
Matches 128; Conservative
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CITY: St. Louis
STATE: Missouri
COUNTRY: USA
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US-08-627-706-5
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US-08-627-706-5
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May 18, 2004, 17:59:12; Search time 141.75 Seconds (without alignments) 4930.226 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                     5894648
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                2947324 segs, 2269024515 residues
                                                                                                                  US-10-681-972-12_COPY_116_269
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Maximum Match 100%
Listing first 45 summaries
                                              OM nucleic - nucleic search, using sw model
                                                                                                                                                              IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                              seq length: 0
seq length: 200000000
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140.2
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Perfect score:
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Maximum DB
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No.
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sult being printed, ribution.		Description	Sequence 14, Appl	Sequence 14, App.	Sequence 12, Appl	Sequence 12, App.	Sequence 9, Appli	Sequence 9, Appl:	Sequence 13, Appl	Sequence 2046, Ap	Sequence 2046, Ap	Sequence 15, Appl	Sequence 607, App	Sequence 48, Appl	Sequence 45, Appl	Sequence 19, Appl
ter than or equal to the score of the result being printed, ived by analysis of the total score distribution.	SUMMARIES	ID	US-09-829-381A-14	US-10-681-972-14	US-09-829-381A-12	US-10-681-972-12	US-09-829-381A-9	US-10-681-972-9	US-09-732-561-13	US-09-938-842A-2046	US-09-938-842A-2046	US-09-732-561-15	US-09-887-576-607	US-09-759-584-48	US-10-388-361A-45	US-10-006-252A-19
gqua]		DB	6	13	σ	13	σ	13	σ	σ	11	σ	σ	σ	13	14
an or e		* Query Match Length DB	270	270	286	286	500	200	403	243	243	400	400	414	414	414
ter th		* Query Match	100.0	100.0	100.0	100.0	91.0	91.0	77.5	76.5	76.5	76.5	76.5	76.5	76.5	76.5

22 2 2 2 2	Sequence 1 equence 1 Sequence 1 equence 5 equence 5	Sequence Sequence Sequence Sequence Sequence Sequence Sequence 1	AMOILGILA.	Sequence 6, Appli Sequence 31, Appli Sequence 31, Appl Sequence 34, Appl Sequence 34, Appl Sequence 48, Appl Sequence 31, Appl
9 US-09-732-561-21 13 US-09-829-381A-5 13 US-10-681-972-5 9 US-09-759-584-58 9 US-09-829-381A-8 13 US-10-681-972-8 9 US-09-829-381A-8	0.681.972.1 0.681.972.1 0.681.972.1 -759.584.50	5 US-10-178-449A-5 US-10-178-449A-5 US-10-178-449A-5 US-10-178-449A-5 US-10-178-449A-6 US-10-178-469A-6 US-10-178-469A-6 US-10-178-489A-6 US-10-178-489A-6 US-10-178-489A-6 US-10-178-480A-6 US-10-178-480A-6 US-10-178-480A-6 US-1	-178-4 -178-4 -178-4 -178-4 -178-4	US-09- US-09- US-09- US-09- US-09- US-1(
1616 308 308 288 306 306	2 2 2 2 2 2 3 3 4 4 3 3 3 4 4 3 3 3 4 4 3 3 3 3	156 610 658 439 457	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	565 150 150 150 150 529
75.5 74.9 73.4 71.8 9.0 9.0	666.8 66.8 66.8 66.8 66.8	28.3 28.3 27.7 27.7	27.7 27.7 27.7 27.7 27.7 27.7	24.5 25.1 25.3 25.3 25.3 25.3
116.2 115.4 115.4 113.0 110.6	102.8 102.8 102.8 102.8 102.8	m m m ci ci c	4 4 4 4 4 4 2 4 4 4 4 4 4 3 6 6 6 6 6 6 7	44 m m m 0 0 0 0 0 4 0 0 0 0 4 0 0 0 0 0
115 116 128 129	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	22 2 2 2 3 3 3 3 4 4 4 4 4 4 4 4 4 4 4 4	1 W W W W W W W W W W W W W W W W W W W	39 44444 10 10 10 10 10 10 10 10 10 10 10 10 10

APPLICANT: Liang, Jihong Shah, Dilip M. Wu, Yonnie S. Rosenberger, Cindy A. TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi Sequence 14, Application US/09829381A Patent No. US20020144306A1 GENERAL INFORMATION: NUMBER OF SEQUENCES: US-09-829-381A-14

ALIGNMENTS

CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NOMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A ZIP: 63198 COMPUTER READABLE FORM: CITY: St. Louis STATE: Missouri COUNTRY: USA

TELECOMMUNICATION INFORMATION: TELEPHONE: (314) 537-6224

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                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG
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                                                                                                                                    APPLICANT: Liang, Jihong
APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
Rosenberger, Cindy A.
TITLE OF INVENTION: Antifugal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 286;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORRENT AGENT INFORMATION:
NAME: COHEN CHARLES E.
REGISTRATION NUMBER: 34,565
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 154; DB 9;
Best Local Similarity 100.0%; Pred. No. 2.4e-42;
Matches 154; Conservative 0; Mismatches 0;
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TOPOLOGY: linear
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MOLECULE TYPE: CDNA
;
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-829-381A-12
                                                                     Sequence 12, Application US/09829381A Patent No. US20020144306A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/10681972; Publication No. US20040064850A1; GENERAL INFORMATION:
APPLICANT: Liang, Jihong; APPLICANT: Shah, Dilip M.; APPLICANT: Wu, Yonnie S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (314) 537-6047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 286 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 63198
                                        US-09-829-381A-12
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US-10-681-972-12
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PUblication No. US20040064850A1
GENERAL INFORMATION
FENERAL INFORMATION
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyasum and Methode for Control TITLE OF INVENTION: Plant Pathogenic Fungi
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/10/681,972
CURRENT FILING DATE: 2003-10-09
FRIOR FILING DATE: 2001-04-09
FRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 CAGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCC 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CAGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCC
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                                                                                                                                                                                                                                                                                                                                                                           Gaps
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100.0%; Score 154; DB 9;
Best Local Similarity 100.0%; Pred. No. 2.3e-42;
Matches 154; Conservative 0; Mismatches 0;
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TELEFAX: (314) 537-6047

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-829-381A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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OTHER INFORMATION: Plasmid
US-10-681-972-14
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LENGTH: 270
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APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu Yonnie W.
APPLICANT: Wu Yonnie W.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control
TITLE OF INVENTION: Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                            91.0%; Score 140.2; DB 9 94.8%; Pred. No. 1.6e-37; iive 0; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 GCTCACAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279 GCTCACAATGTATTTGTTACTTCCCATGTTAA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 GCTCACAAATGTATTGTTACTTCCCATGTTAA 154
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CURRENT APPLICATION NUMBER: US/10/681,972
CURRENT FILING DATE: 2003-10-09
PRIOR APPLICATION NUMBER: US/09/829,381D
PRIOR APPLICATION NUMBER: US/09/829,381D
PRIOR APPLICATION NUMBER: US/09/829,381D
PRIOR FILING DATE: 2001-04-09
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFFWARE: Patentin version 3.1
                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: CDNA SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTHER INFORMATION: N = any nucleotide US-10-681-972-9
            TELEFHONE: (314) 537-6224
TELEFAX: (314) 537-6047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/10681972
Publication No. US20040064850A1
GENERAL INFORMATION:
                                                     INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 94.8
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 145; Conservative
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ORGANISM: Alyssum spp
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Best Local Similarity
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US-10-681-972-9
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LENGIH: 500
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APPLICANT: Rosenberger, Cindy A.

TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control TITLE OF INVENTION: Plant Pathogenic Fungi
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/10/681,972
CURRENT APPLICATION NUMBER: US/09/829,381D
PRIOR PILING DATE: 2003-10-09
PRIOR PLING DATE: 2001-04-09
PRIOR PLING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARER: Patentin Version 3:1
SEQ ID NO 12
LENGTH: 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 CAGGAACCAATGCAGAAACCTTGAAAGAGCAGAAACACGGATCTTGCAACTATGTCTTCCC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 AAGGTTGTGCGAGAGCAAGTGGGAACATGGTCAGGAGTTTGTGGGAACAACAATGCATG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CAGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AAGGTTGTGCGAGAGCCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG
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TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 286;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 154; DB 13; Best Local Similarity 100.0%; Pred. No. 2.4e-42; Matches 154; Conservative 0; Mismatches 0;
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REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               FEATURE:

CHER INFORMATION: Synthetic PCR reaction product US-10-681-972-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 AGCTCACAAATGTATTTGTTACTTCCCATGTTAA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 AGCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
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APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/103,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/09829381A
Patent No. US20020144306A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1998-06-24 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63198
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US-09-829-381A-9
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Sequence 2046, Application US/09938842A

Fatent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHOD OF USE

FILE REFERENCE: SCRIP1300-3

CURRENT FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: S379

SEQ ID NO 2046

LENGTH: 243
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Sequence 2046, Application WS/09938842A

Publication No. US20040009476A9

GENERAL INFORMATION:
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICATION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS
CURRENT FILING DATE: 2001-08-24
FILE REFERENCE: SCRIP1300-3
CURRENT FILING DATE: 2001-08-24
FRIOR PILING DATE: 2001-08-24
FRIOR PILING DATE: 2001-01-16
FRIOR PILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: S379

SEQ ID NO 2046

LENGTH: 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 117.8; DB 9; Length Pred. No. 5.3e-30; 0; Mismatches 22; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 85.6%;
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
US-09-938-842A-2046
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  US-09-938-842A-2046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/202,638
APPLICATION NUMBER: 09/202,638
                                                                                                                                                                                  APPLICANT: Thomma, Bart
APPLICANT: Thomma, Bart
APPLICANT: Perras, Franky
APPLICANT: Penninckx, Iris
APPLICANT: Manners, John
APPLICANT: Razan, Kemal
APPLICANT: Razan, Kemal
APPLICANT: Broekaert, Willem
TITLE OF INVENTION: Plant Protection Method
NUMBER OF SEQUENCES: 24
CORRESONDENCE ADDRESS:
ADDRESSEE: ZENECA AG Products
STREET: 1800 Concord Pike
CITY: Wilmington
STATE: Wilmington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
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279 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/01672
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, 1.12a D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: PPD 50165/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-1699
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                     US-09-732-561-13
; Sequence 13, Application US/09732561
; Patent No. US20020035738A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 403 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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Best Local Similarity
Matches 132; Conserv
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                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Thomma
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MOLECULE TYPE: CI
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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Gaps 0 22; Indels 76.5%; Score 117.8; DB 1. 85.6%; Pred. No. 5.3e-30; cive 0; Mismatches 22 Query Match Best Local Similarity 85.6 Matches 131; Conservative

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182 AAGAATCAGTGCATTAACCTTGAAGGAGCCAAACATGGATCATGCAACTATGTCTTCCCA 241
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                                                                                                                                                                                                                                                                                                                       APPLICANT: Brown, D.
APPLICANT: Brown, D.
APPLICANT: Chang, H.
APPLICANT: Chang, H.
APPLICANT: APPLICANT: Brown, D.
APPLICANT: Han, B.
APPLICANT: Han, B.
APPLICANT: Wang, X.
APPLICANT: Wang, X.
APPLICANT: Cooper, Bret
TITLE OF INVENTION: Promoters for regulation of plant expression CURRENT APPLICATION NUMBER: US/09/887,576
CURRENT APPLICATION NUMBER: US/09/887,576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
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                                                                                                                                         242 GCACACAAGTGTATCTGTTACGTCCCATGTTAA 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
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                                                                                             122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR APPLICATION NUMBER: US 60/258,692
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 875
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 48, Application US/09759584
; Patent No. US200100101432A1
GENERALINFORMATION:
APPLICANT: BROEKAERT, MILLEM F.
APPLICANT: CAMMUE, BRIND P.A.
APPLICANT: CAMMUE, REST W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.C.
APPLICANT: TERRAS, FRANKY R.C.
APPLICANT: TENDELLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
                                                                                                                                                                                                                                                          Sequence 607, Application US/09887576
Patent No. US20020144047A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (1)...(400)
; OTHER INFORMATION: n = A,T,C
US-09-887-576-607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
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                                                                                                                                    151 AAGAATCAGTGCATTAACCTTGAAGGAGCCAAACATGGATCATGCAACTATGTCTTCCCA 210
                                         91 AAGTIGIGIGAGAAGICIAAGIGGAAAIGGICAGGGGITIGCGGAAACAGIAAIGCAIGC 150
    61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 AGGITGIGCGAGAGACCAAGIGGGACAIGGICAGGAGITIGIGGAACAACAAIGCAIGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732,561
                                                                                                                                                                                                                                                                                                                                           Sequence 15, Application US/09732561
Fatent No. US20020035738A1
GENERAL INPORMATION:
APPLICANT: Terras, Franky
APPLICANT: Penninckx, Iris
APPLICANT: Manners, John
APPLICANT: Broakert, Willem
TITLE OF INVENTION: Plant Protection Method
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                211 GCACACAAGTGTATCTGTTACGTCCCATGTTAA 243
                                                                                                                                                                                     122 GCTCACAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/01672
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hohenschutz, ilza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: PPD 50165/UST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 886-1699
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PARIOR ARPLICATION DATA:
PAPLICATION NUMBER: 09/202,638
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSEE: ZENECA Ag Products
I: 1800 Concord Pike
Wilmington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 76.5%;
Best Local Similarity 85.6%;
Matches 131; Conservative
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CI
ORIGINAL SOURCE:
STRAIN: PDF1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
STREET: 18
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US-09-732-561-15
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US-09-732-561-15
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STATE: D
COUNTRY:
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62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 AAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 76.5%; Score 117.8; DB 13; Length Best Local Similarity 85.6%; Pred. No. 6.6e-30; Matches 131; Conservative 0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 76.5%; Score 117.8; DB 14; Length Best Local Similarity 85.6%; Pred. No. 6.6e-30; Matches 131; Conservative 0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   226 GCTCACAAGTGTATCTGCTACTTTCCTTGTTAA 258
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                        CURRENT APPLICATION NUMBER: US/10/388,361A
CURRENT FILING DATE: 2003-03-13
PRIOR PRILOR APPLICATION NUMBER: US 09/077,948
PRIOR PRILOR APPLICATION NUMBER: PCT/GB96/03068
PRIOR FILING DATE: 1996-12-12
PRIOR PILING DATE: 1996-12-12
PRIOR APPLICATION NUMBER: GB 9606552.9
PRIOR PILING DATE: 1996-03-28
PRIOR PILING DATE: 1996-03-28
PRIOR PILING DATE: 1995-12-13
NUMBER: OF SEQ ID NOS: 141
SOUTHARE: FASTERQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: De Samblanx, Genoveva
APPLICANT: Broekaert, Willem
APPLICANT: Broekaert, Willem
APPLICANT: Rees, Sarah
TITLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: SYN-034DV
CURRENT APPLICATION NUMBER: US/10/006,252A
CURRENT FILING DATE: 2001-12-04
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: GB 9525474.4
PRIOR FILING DATE: 1996-12-13
PRIOR FILING DATE: 1996-12-13
PRIOR FILING DATE: 1996-12-13
NUMBER OF SEQ ID NOS: 77
SECTRARRE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19, Application US/10006252A Publication No. US20020152498A1
    FILE REFERENCE: 50094PPDDIV
                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Raphanus sativus
US-10-388-361A-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA; ORGANISM: Raphanus sativus
US-10-006-252A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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US-10-006-252A-19
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                                                                                                                                                         ZIP: 20005
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99042/SEE.36525/US/A
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NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Antifungal Proteins
                                                                                                                                                                                                                                                                                                                                                 PILING DAIE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/377,687
FILING DATE:
ATTONNEY/ABENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/POCKET NUMBER: 99042/S
TELECOMMUNICATION INFORMATION:
TELEPONE: 202-861-3000
TELEFAX: 202-861-3000
TELEPONE: 202-861-3000
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs
INFORMATION CHARACTERISTICS:
LENGTH: 414 base pairs
STRANDENSS: both
TOPOLOGY: linear
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 45, Application US/10388361A
Publication No. US20030226169A1
GENERAL INFORMATION:
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Broekaert, Willem
Van Gelder, Wilhelmus
Rees, Sarah
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Sitjtsma, Lolke
Meloen, Robbert
Puijk, Wouter
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APPLICANT: Fant, Franky
APPLICANT: Borremans, Frans
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LOCATION: 16..255
                                                                                          WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-388-361A-45
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                                                                                                                                        COUNTRY:
                                                                                          CITY: W
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 19850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/09/732,561
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Thomma, Bart
APPLICANT: Terras, Franky
APPLICANT: Penninckx, Iris
APPLICANT: Penninckx, Iris
APPLICANT: Manners, John
APPLICANT: Kazan, Kemal
APPLICANT: Rocedeart, Willem
TITLE OF INVENTION: Plant Protection Method
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: ZENECA AG Products
STREET: 1800 Concord Pike
CITY: Wilmington
STATE: DE
COUNTRY: USA
    122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                                                  226 GCTCACAGAGTGTATCTGCTACTTTCCTTGTTAA 258
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MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: Arabidopsis PDF1.2 gene
INDIVIDUAL ISOLATE: DNA sequence Figure 14
US-09-732-561-21
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PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/202,638
FILLING DATE:
FILLING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PC-UUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: HORDMENCH, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: PPD 50165/UST
TELECHONICATION INFORMATION:
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Patent No. US20020035738A1
GENERAL INFORMATION:
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Db 1535 GCACACAAGTGTATCTGTTACGTCCCATGTTAA 1567
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Search completed: May 18, 2004, 20:33:21 Job time : 141.75 secs man min min man

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Run on: ĕ

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    (without alignments)
3225.394 Million cell updates/sec
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           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                          nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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                                                                                                                               Title:
Perfect score:
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Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Gaps

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Indels

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APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control TITLE OF INVENTION: Plant Pathogenic Fungi
FILE REPERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/10/681,972
CURRENT PILING DATE: 2003-10-09
PRIOR FILING DATE: 2001-04-09
PRIOR PAPLICATION NUMBER: 09/103,489
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 12
LENGTE: 286
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                                                                                                                                                                                                108 AAGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATG
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                                                                                                                 100.0%; Score 154; DB 53;
100.0%; Pred. No. 7.1e-39;
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100.0%; Pred. No. 7.3e-39;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                           228 AGCTCACAATGTATTTGTTACTTCCCATGTTAA 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 AGCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
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                                                                                                                                                                                                                                                                                                                                                                                  US-10-681-972-12; Sequence 12, Application US/10681972; GENERAL INFORMATION:
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                             TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
                                                                        OTHER INFORMATION: Plasmid
                                                                                                                Query Match
Best Local Similarity 100.
Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    al Similarity 100.
154; Conservative
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SEQ ID NO 14
LENGTH: 270
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APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Wosenberger, Cindy A.
TITLE OF INVENTION: Attifungal Polypeptide ALYAFP from Alyssum and Methods for Contro TITLE OF INVENTION: Plant Parthogenic Fungi
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/10/681,972
CURRENT FILING DATE: 2003-10-09
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
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13, Appl
117133,
117133,
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Sequence 19, Appl
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Sequence 48, Appl
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Sequence
Sequence
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Sequence
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                                                     US-09-759-584-48
US-10-006-252A-19
US-10-388-361A-45
US-09-694-619-132225
US-09-684-016-132225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-681-972-14; Sequence 14, Application US/10681972; GENERAL INFORMATION:
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                                                                                                                                                                                                      61290
61290
87080
87080
243
243
243
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154
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122.6
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122.6
122.6
122.6
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122.6
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0

Gaps

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Indels

Length 286;

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CELLS, AND METHODS THEREOF CAPABLE
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              91 AAGTIGIGCGAGAAGCCAAGIGGIACTIGGICAGGAGTITGCGGAAACAGCAAIGCAIGC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
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                                                                62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA
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TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES,
TITLE OF INVENTION: MODULATING VARIOUS RESPONSES
FILE REFERRNCE: 2750-1481P
CURRENT APPLICATION NUMBER: US/09/935,625
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO S.250
LENGTH: 243
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TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES,
TITLE OF INVENTION: MODULATING VARIOUS RESPONSES
FILE REFERENCE: 2750-1481P
CURRENT APPLICATION NUMBER: US/09/935,625
CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.6%; Score 122.6; DB 38
87.6%; Pred. No. 9.8e-29;
Live 0; Mismatches 19,
                                                                                                                                                           GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                       211 GCTCACAAGTGTATCTGTTACGTCCCATGTTAA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211 GCTCACAATGTATCTGTTACGTCCCATGTTAA 243
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; LOCATION: 1..243
; OTHER INFORMATION: Ceres Seq. ID no. 2711695
US-09-935-625-5383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Ceres Seq. ID no. 2143607
US-09-935-625-5250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Arabidopsis thaliana
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Best Local Similarity 87.67
Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Misc feature
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Best Local Similarity
Matches 134; Conserva
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LENGTH: 243
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APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: W. Younie S.
APPLICANT: W. Younie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Plant Pethogenic Fungi
FILE OF INVENTION: Plant Pethogenic Fungi
FILE REFERENCE: 38-21 (10700) C.
CURRENT APPLICATION NUMBER: US/10/681,972
CURRENT FILING DATE: 2003-10-09
PRIOR PILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR PILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: N. ALEXANDROV et al.
TITLE OF INVANDATION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243F
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 18199
LENGTH: 243
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Pred. No. 2.5e-34;
0; Mismatches 8; Indels 0;
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NAME/KEY: misc feature

LOCATION: 1..243

OTHER INFORMATION: any n = a, g, c, t, unknown, or other

NAME/KEY: misc feature

LOCATION: 1..243

OTHER INFORMATION: Ceres Seq. ID 1833757

US-09-708-427-18199
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; OTHER INFORMATION: N = any nucleotide
US-10-681-972-9
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity 94.8%;
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Alyssum spp
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. USSN 60/120,645 1999-02-18; USSN 09/443,025 1999-11-1; USSN 60/120,645 1999-02-18; USSN 09/443,025 1999-11-12;
                                                                                                                                 151 AAGAATCAGIGCATTAACCTTGAAGGAGCAAAACATGGATCTTGCAACTATGTCTTCCCA 210
                                                                                                                                                                             62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
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                                                     Gaps
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APPLICANT: Timberlake, William E.
TITLE OF INVENTION: Plant Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15478)B
CURRENT PELLING DATE: 0200-02-16
PRIOR APPLICATION NUMBER: US/09/505,532
PRIOR APPLICATION NUMBER: USSN 60/120,645 1999-02-18; USSN 0
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      Score 122.6; DB 38; Length 243; Pred. No. 9.8e-29;
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APPLICANT: Timberlake, William E.

TITLE OF INVENTION: Plant Genome Sequences and Uses Thereof FILE REFERENCE: 38-00(15478) B.

CURRENT APPLICATION NUMBER: US/09/819,091A

CURRENT FILING DATE: 2000-02-16

PRIOR FILING DATE: 1998-11-16

PRIOR FILING DATE: 1998-11-12

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-11-12

WUMBER OF SEQ ID NOS: 51470

SEQ ID NO 7439

LENGTH: 584

TYPE: DNA
                                                  0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                       122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
                                                                                                                                                                                                                                                                                                            211 GCTCACAAGTGTATCTGTTACGTCCCATGTTAA 243
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10.09-819-091A-7439/c

3. Sequence 7439, Application US/09819091A

3. GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
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; ORGANISM: Arabidopsis thaliana
US-09-505-532-7439
    Query Match
Best Local Similarity 87.6%;
Matches 134; Conservative
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SEQ ID NO 7439
LENGTH: 584
Query Match
Best Local Similarity
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Best Local Similarity
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Matches 134;
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE
TITLE OF INVENTION: MODULATING VARIOUS RESPONSES
FILE REFERENCE: 2750-1441P
CURRENT APPLICATION UNMERR: US/09/935,625
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 28943
                                                                                                                                                                                                                                                                                                                                                                                                                      CELLS, AND METHODS THEREOF CAPABLE
                                                                                                                                                 151 AAGAATCAGTGCATTAACCTTGAAGGAGCAAAACATGGATCTTGCAACTATGTCTTCCCA 210
                                                            62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
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                         61
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                                                                                                                                                                                                                                                                                                                                          Sequence 28557, Application US/09935625
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: POLYNCLECTIDES, POLYPEPTIDES,
TITLE OF INVENTION: MODULATING VARIOUS RESPONSES;
FILE REFERENCE: 2750-1481P;
CURRENT APPLICATION NUMBER: US/09/935,625
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 28557
LENGTH: 243
                                                                                                                                                                                                                        211 GCTCACAAGTGTATCTGTTACGTCCCATGTTAA 243
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| LOCATION: 1...243

| TOTER INFORMATION: Ceres Seq. ID no. 2143607

US-09-935-625-28557
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; LOCATION: 1...243
; CTHEN OTHEN CERES Seq. ID no. 2711695
US-09-935-625-28943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Arabidopsis thaliana
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity
                                                                                                                                                                                                                                                                                                       RESULT 7
US-09-935-625-28557
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US-09-534-859-284/c
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GENERAL INFORMATION:
APPLICANT: Bush, David F.
APPLICANT: Levin, Irena M.
APPLICANT: Levin, Irena M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Rounsley, Steven D.
APPLICANT: Rounsley, Steven D.
APPLICANT: Wiegand, Roger C.
ITLE OF INVENTION: PLANT POLYMORPHIC MARKERS AND USES THEREOF FILE REPERBENCE: 38-10(15493)B
CURRENT APPLICATION NUMBER: US/09/534,859
CURRENT FILING DATE: 2000-229
1000 The CORRENT FILING DATE: 2000-229
11177
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                                                                                                                                                     GTGGGAACAACAATGCATGC
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                                                                   DB 33; Length 584;
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APPLICANT: Levin, Irena M.
APPLICANT: Norris, Susan R.
APPLICANT: Nounsley, Steven D.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof FILE REPERENCE: 38-10(15493) D.
CURRENT APPLICATION NUMBER: US/09/803,736
CURRENT PILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 09/534,859
                                                              Score 122.6; DB 33; Length
Pred. No. 1.3e-28;
0; Mismatches 19; Indels
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Pred. No. 6.2e-28;
0; Mismatches 19; Indels
                                                                                                                                                   2 AGGTTGTGCGAGAGACCAAGTGGGACATGGTCAGGAGTT
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ORGANISM: Arabidopsis thaliana
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CRGANISM: Arabidopsis thaliana
US-09-534-859-830
                                                              79.6%;
87.6%;
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Best Local Similarity 87.6%;
Matches 134; Conservative
                                                                                Best Local Similarity 87.6
Matches 134; Conservative
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    ; ORGANISM: ATADIC
US-09-819-091A-7439
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US-09-803-736-830/c
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LENGTH: 61290
                                                              Query Match
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: identified by Attorney Docket number 04983.0206CPUS01 38-10.
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 1582
SEQ ID NO 830
LENGTH: 61290
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APPLICANT: Levin, Irena M.
APPLICANT: Levin, Irena M.
APPLICANT: Norris, Susan R.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parnell, Laurence D.
APPLICANT: Rounsley, Steven D.
APPLICANT: Rounsley, Steven D.
APPLICANT: Rounsley, Steven D.
APPLICANT: Rounsley, Steven D.
APPLICANT: Rounsley, Steven D.
APPLICANTON: 38-10(15493)B
CURRENT APPLICATION NUMBER: US/09/534,859
CURRENT FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 1127
                                                                                                                                                                                                                                                                              Query Match 79.6%; Score 122.6; DB 33; Length 61290; Best Local Similarity 87.6%; Pred. No. 6.2e-28; Matches 134; Conservative 0; Mismatches 19; Indels 0;
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87.6%; Pred. No. 6.9e-28;
Nismatches 19;
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; Sequence 284, Application US/09803736
; GENERAL INFORMATION:
                                                                                                                                                                                            ; ORGANISM: Arabidopsis thaliana
US-09-803-736-830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Arabidopsis thaliana US-09-534-859-284
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Best Local Similarity 87.6'
Matches 134; Conservative
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APPLICANT: Levin, Irena M.
APPLICANT: Norris, Susan R.
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211 GCTCACAAGTGTATCTGTTACTTCCCATGTTAA 243

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Search completed: May 18, 2004, 20:22:42 Job time : 1681 secs
         d
APPLICANT: Rounsley, Steven D.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
FILE REPERENCE: 38-10(15493)D
CURRENT APPLICATION NUMBER: US/09/803,736
CURRENT FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: 12000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-10-20
RIOR APPLICATION NUMBER: identified by Attorney Docket number 04983.0206CPUS01 38-10
NUMBER OF SEQ ID NOS: 1582
SEQ ID NO 284
LIENGTH: 87080
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US-09-708-427-21472

SEQUENCE 21472.

SEQUENCE 21472.

GENERAL INCORMATION:

TITLE OF INVENTION: THEREBY

FILE REFERENCE: 2750-1243P

CURRENT APPLICATION UNMER: US/09/708,427

CURRENT APPLICATION UNMER: 2000-11-09

NUMBER OF SEQ ID NOS: 85564

SEQ ID NOS: 82644

SEQ ID NOS: 1472

LENGTH: 243
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                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 79.6%; Score 122.6; DB 33; Length Best Local Similarity 87.6%; Pred. No. 6.9e-28; Matches 134; Conservative 0; Mismatches 19; Indels
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COCATION: 1..243

OTHER INFORMATION: any n = a, g, c, t, unknown, or other;
NAME/KEY: misc_feature

COCATION: 1..243

OTHER INFORMATION: Ceres Seq. ID 1839548

US-09-708-427-21472
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                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-803-736-284
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Best Local Similarity 86.34
Matches 132; Conservative
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151 AGAATCAGTGCATTAACCTTGAGGGGGAAAACATGGATCTTGCAACTATGTCTTCCCA 210

GCTCACAAATGTATTGTTACTTCCCATGTTAA 154

122

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US-10-767-471-10730/c
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OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-:
US-10-767-471-10730
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOODISOS
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT APPLICADATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FASLERQ for Windows Version 4.0
SEQ ID NO 10730
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      Sequence 11946, A Sequence 8785, Ap Sequence 12265, Ap Sequence 21234, A Sequence 25146, A Sequence 1550, Ap Sequence 12564, A Sequence 12564, A Sequence 22795, A Sequence 22795, A Sequence 22795, A Sequence 21570, A Sequence 21570, A Sequence 21570, A Sequence 21570, A Sequence 1159, A Sequence 1159, A Sequence 1159, A Sequence 6153, A Sequence 12169, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequence 6153, A Sequen
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Sequence 151, Application US/10417375A

GENERAL INFORMATION:

APPLICANT: David W. Morris

APPLICANT: Marc Malandro

TITLE REPERENCE: 529452001600

FILE REPERENCE: 529452001600

GURRENT APPLICATION UNMERR: US/10/417,375A

CURRENT FILING DATE: 2003-04-15
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US-10-796-307-8785
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US-10-796-280-12394
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9183 AAGGCTCAGCTACATACCAAGGGCAACCTGGTGGTGGTAGTTCCATCAGAGGTC 9124
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GRNERAL INFORMATION:
APPLICAMT: CARGILL.
AITLE CARFILL.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001524
CURRENT APPLICATION NUMBER: US/60/568,845
CURRENT FILING DATE: 2004-05-07
NUMBER OF SEQ ID NOS: 39608
SOFTWARE: FARESEQ for Windows Version 4.0
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0.26;
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Sequence 151, Application US/10417375B
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: David W. Morris
TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
FILE REFERENCE: 52945200160
CURRENT APPLICATION NUMBER: US/10/417,375B
CURRENT FILING DATE: 2003-04-15
NUMBER OF SEQ ID NOS: 176
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 151
INNER 1200
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22.5%; Score 34.6; Di
Best Local Similarity 59.8%; Pred. No. 0.26
Matches 58; Conservative 0; Mismatches
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NUMBER OF SEQ ID NOS: 176
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 151
LENGTH: 42063
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; OTHER INFORMATION: n = A,T,C or G
US-10-417-375A-151
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; NAME/KEY: misc feature
LOCATION: (1)...(42063)
; CTHER INFORMATION: n = A,T,C or G
US-10-417-375B-151
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Best Local Similarity 59.89
Matches 58, Conservative
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CARGLL, Michele et al.
TITLE OF INVENTION: STENCES, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: STENCES, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION WNBER: US/60/568,845
CURRENT APPLICATION WNBER: 2004-05-07
NUMBER OF SEQ ID NOS: 39608
SOFTWARE; FastSEQ for Windows Version 4.0
IENGTH: 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: CARGILL, Michele et al.
TITLE DE INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE DE INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01524
CURRENT APPLICATION NUMBER: US/60/568,845
CURRENT FILING DATE: 2004-05-07
NUMBER OF SEQ ID NOS: 39608
SOFTWARE: FASTSEQ for Windows Version 4.0
LENGTH: 201
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                                                                                                             DB 7; Length 201;
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62.0%; Pred. No. v...
0; Mismatches
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Pred. No. 0.51;
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                                                                                                       Query Match
Best Local Similarity 62.04
Matches 49; Conservative
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Matches 49; Conservative
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-568-845-22848
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; ORGANISM: Homo sapiens
US-60-568-845-22851
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CORGANISM: Homo sapiens
US-60-568-845-22854
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US-60-568-845-22854
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DB 7;
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20.1%; Score 31; DB 7
Best Local Similarity 62.0%; Pred. No. 6.4;
Matches 49; Conservative 0; Mismatches
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Matches 46; Conservative
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NAME/KEY: misc_feature
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US-60-568-845-22832
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LENGTH: 201
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82 AAGGAAGGAAGGAAGGAAGAAGAAAAAAAAAGAGGAAAACAGAAACATTGCAACAAT 141
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GENERAL INFORMATION:
APPLICAMY: CARGILL, Michele et al.
TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STEAMSIS, METHODS OF DETECTION AND USES THEREOF
FULE REFERENCE: CLOO1524
CURRENT APPLICATION NUMBER: US/60/568,845
CURRENT FILING DATE: 2004-05-07
NUMBER OF SEQ ID NOS: 39608
SOFTWARE: FASTSEQ for Windows Version 4.0
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Thes 30; Indels
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                                                                                                                                                                                                                          APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASS
TITLE OF INVENTION: STENOSIS, METHODS OF DE:
FILE REPRENCE: CLOO1524
CURRENT APPLICATION NUMBER: US/60/568,845
CURRENT FILING DATE: 2004-05-07
NUMBER OF SEQ ID NOS: 39608
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22856
                                                                                                                                                                                       Sequence 22856, Application US/60568845 GENERAL INFORMATION:
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                                                                                  142 GACTACTGAGTTGGAAGAT 160
                                           113 GTCTTCCCAGCTCACAAAT 131
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49; Conservative
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Best Local Similarity 62.0%
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ORGANISM: Homo sapiens
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SNGTH: 201
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Matches
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1 LOCATION: (1)...(96902)
2 OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-2
US-60-568-845-2915
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOUISS4
CURRENT APPLICATION NUMBER: US/60/568,845
CURRENT FILING DATE: 2004-05-07
NUMBER OF SEQ ID NOS: 39608
SOFTWARE: FASTERO for Windows Version 4.0
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US-60-568-845-22842

) Sequence 22242.

) GENERAL INFORMATION:

) APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

) FILE REFERENCE: CLOO1524

) CURRENT APPLICATION NUMBER: US/60/568,845

) CURRENT FILING DATE: 2004-05-07

) NUMBER OF SEQ ID NOS: 39608
                                                               DETECTION AND USES THEREOF
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APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND US
FILE REFERENCE: CLOOLS24
CURRENT APPLICATION NUMBER: US/60/568,845
CURRENT FILING DATE: 2004-05-07
NUMBER OF SEQ ID NOS: 39608
SOFTWARRE: FASLESQ for Windows Version 4.0
SEQ ID NO 2915
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GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DeNIES, Sue K.
APPLICANT: CHARTERIS, Paul
APPLICANT: ROSENRELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
TITLE OF INVENTION: COMPOSITIONS, METHODS, AND SYSTEMS FOR INFERRING BOVINE BREED
FILE REPERENCE: MMILLSOWO
CURRENT FILING DATE: 2003-12-31
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOIS24
CURRENT APPLICATION NUMBER: US/60/568,845
CURRENT FILING DATE: 2004-05-07
NUMBER OF ESQ ID NGS: 39608
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22830
LENGTH:: 201
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Best Local Similarity 53.3%; Pred. No. 1.7;
Matches 64; Conservative 0; Mismatches 56; Indels 0
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Best Local Similarity 53.3%; Pred. No. 1.7;
Matches 64; Conservative 0; Mismatches 56; Indels 0
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PCT-US03-41761-31797/c
· Semience 31797, Application PC/TUS0341761
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PRIOR FILING DATE: 2002-12-31
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PCT-US03-41761-31797
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SOFTWARE: PatentIN version 3.1
SEQ ID NO 31797
LENGTH: 1207
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; ORGANISM: Homo sapiens
US-60-568-845-22830
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Best Local Similarity
Matches 45; Conserv
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MAI GENOMICS, INC.
APPLICANT: DeNISE, Sue K.
APPLICANT: CHARTERIS, Paul
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
ITLE OF INVENTION: COMPOSITIONS, METHODS, AND SYSTEMS FOR INFERRING BOVINE BREED
FILE REFERENCE: MAIL150WO
CURRENT APPLICATION NUMBER: PCT/US03/41761
CURRENT APPLICATION NUMBER: US 60/437,482
PRIOR APPLICANION NUMBER: US 60/437,482
PRIOR PILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIN version 3.1
SEQ ID NO 3197
LENGTH. 1207
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001524
CURRENT APPLICATION NUMBER: US/60/568,845
CURRENT FILING DATE: 204-05-07
NUMBER OF SEQ ID NOS: 39608
SOFTWARE: FASTSEQ for Windows Version 4.0
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Pred. No. 0.83;
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 22842
LENGTH: 201
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ORGANISM: Bovine 19866880664695
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1 Similarity 63.9%;
46; Conservative
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Matches 46; Conservative
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                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-568-845-22842
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; ORGANISM: Homo sapiens
US-60-568-845-22845
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Best Local Similarity
Matches 46; Conserv
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US-60-568-845-22845
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Search completed: May 18, 2004, 20:26:20 Job time: 71.55 secs

BN45.040D BN25.067G BN40.059J BN45.040H BN40.0630 BN45.0409 BN45.0430 BN45.0430 BN45.0430 BN45.0430 BN45.0430 BN45.0430

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CD832609 BN45.040H
CD834994 BN45.0430
CD834109 BN45.0430
CD83169 BN40.060H
CD831014 BN40.060H
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CD831464 D801 G8N
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BG321454 D801 G8N
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BG311515 Ds01 08a0
CA992140 HCO577 GI
CD831226 BN40.0584
CD831925 BN45.0430
CD83784 BN45.0401
CD834095 BN45.0401
CD833924 BN45.0401
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Peprandophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genoplante, a major partnership french program in plant genomics Unpublished (2003)
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                                         CD833983
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Brassica napus
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Genoplante
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KEYWORDS
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TITLE
JOURNAL
COMMENT
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CD832625
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CD834168 BN45.040N
CD833944 BN45.040B
CD826491 BN25.064A
                                                                                  May 18, 2004, 17:05:11 ; Search time 1282.4 Seconds (without alignments) 3586.070 Million cell updates/sec
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       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                             27513289 segs, 14931090276 residues
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Maximum Match 100%
Listing first 45 summaries
                                                            nucleic search, using sw model
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CD833944 420 bp mRNA linear EST 10-JUL-2003
BN45.040B07F011019 BN45 Brassica napus cDNA clone BN45040B07, mRNA
sequence.
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BN25.064A05F020416 BN25 Brassica napus cDNA clone BN25064A05, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 AGGAACCAAIGCAGAAACCIIGAAAGAGCAGAACACGGAICTIGCAACIAIGICTICCCA 121
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Brassica napus
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 421)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Tel: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com
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Genoplante, a major partnership french program in plant genomics Unpublished (2003)
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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                                   154
                                                     260 GCTCACAAGTGTATTTGCTACTTCCCTTGTTAA 292
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87.6%; Pred. No. 6.2e-27;
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                           122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA
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/clone="BN45040B07"
/tissue_type="seed"
/clone_lib="BN45"
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CD833944.1 GI:32515884
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CD826491.1 GI:32508431
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Brassica napus
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Genoplante
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CD833944
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BN45.040N06F011018 BN45 Brassica napus cDNA clone BN45040N06, mRNA
                                                                                                                                                                                                                                                                           143 AAGTIGIGCGAGAGGCCAAGIGGGACAIGGICAGGAGICTGIGGAAACAAIAACGCAIGC 202
                                                                                                                                                                                                                                                                                                                  62 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 121
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Mkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
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Contact: Genoplante
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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                                                                                                                                                                                                                                                                                                                                                                                         122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA
organism="Brassica napus"

    419
    /organism="Brassica napus"
/mol_type="mRNA"
    /cultivar="Jet neuf"

             /mol_type="mRNA"

cultivar="Jet neuf"

/db xref="taxon:3708"

clone="BM40064A14"

tissue type="seed"

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CD834168
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BN45.040D05F011019 BN45 Brassica napus CDNA clone BN45040D05, mRNA sequence.
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                                                                                                                                                                                                                                                            201 AAGAATCAGTGCATTAACCTTGAAAAAGCACGACATGATCTTGCAACTATGTCTTCCCA 260
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosdids; eurosids II; Brassicales; Brassicaceae; Brassica.

    (bases 1 to 421)

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Fax: 33 1 69 47 54 10
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Unpublished (2003)
Contact: Genoplante
Genoplante
                                                                                                                                        141 AAGTIGIGCGAGAGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC
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                                                       Score 122.6; DB 14;
Pred. No. 6.2e-27;
0; Mismatches 19;
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87.6%; Pred. No. 6.2e-27;
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                                                     Query Match
Best Local Similarity 87.6%;
Matches 134; Conservative
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Matches 134; Conservative
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                                                                                                      93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
                      Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
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Tel: 33 1 69 47 54 00
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79.6%; Score 122.6; DB 14; Length 421;
Best Local Similarity 87.6%; Pred. No. 6.2e-27;
Matches 134; Conservative 0; Mismatches 19; Indels 0;
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CD831111.1 GI:32513051
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BN25.067G02F020123 BN25 Brassica napus CDNA clone BN25067G02, mRNA
Bequence.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
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Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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1-1: 33 1 69 47 54 00

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and http://genoplante-info.infobiogen.fr).
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                                                                                                1. .422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 GCTCACAAGTGTATTTGCTACTTCCCTTGTTAA
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CD827413.1 GI:32509353
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Brassica napus
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Best Local Similarity 87.6
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CD827413
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          CD831972 422 bp mRNA linear EST 10-UUL-2003 BN40.061108F011228 BN40 Brassica napus cDNA clone BN40061108, mRNA
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BN45.040D11F011019 BN45 Brassica napus CDNA clone BN45040D11, mRNA
sequence.
                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosida; eurosida II; Brassicales; Brassicaceae; Brassica.
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Whyaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosida II; Brassicales; Brassicaceae; Brassica.
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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Location/Qualifiers
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Tel: 33 1 69 47 54 00
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Pred. No. 6.2e-27;
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CD831972.1 GI:32513912
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Brassica napus
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Best Local Similarity 87.6%;
Matches 134; Conservative (
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Erassica napus
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales, Brassicaceae, Brassica.
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BN40.063015F011228 BN40 Brassica napus cDNA clone BN40063015, mRNA
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Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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Contact: Genoplante
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Genoplante, a major partnership french program in plant
Unpublished (2003)
Contact: Genoplante
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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CD832592.1 GI:32514532
                  Brassica napus (rape)
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BN40.059J13F011208 BN40 Brassica napus cDNA clone BN40059J13, mRNA
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BN45.040H17F011019 BN45 Brassica napus cDNA clone BN45040H17, mRNA
                                                                 62 AGGAACCAATGCAGAAACCITGAAAGAGCAGAACACGGATCTTGCAACTATGTTTCCCA 121
                                                                                                         201 AAGAATCAGTGCATTAACCTTGAGAAGCACGACATGGATCTTGCAACTATGTTTCCCA 260
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
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Contact: Genoplante
Genoplante
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79.6%; Score 122.6; DB 14; Length 438;
Best Local Similarity 87.6%; Pred. No. 6.2e-27;
Matches 134; Conservative 0; Mismatches 19; Indels 0;
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CD831479.1 GI:32513419
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/organism="Brassica napus"

Location/Qualifiers

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GI:32516008

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RESULT 11 CD834068

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122 GCTCACAAATGTATTTGTTACTTCCCATGTTAA 154
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BN40.061003F011227 BN40 Brassica napus cDNA clone BN40061003, mRNA
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Genoplante.
Genoplante, a major partnership french program in plant genomics
Uppublished (2003)
Contact: Genoplante
Genoplante
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Location/Qualfilers
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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BN45.040E18F011019 BN45 Brassica napus CDNA clone BN45040E18, mRNA
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BN45.043006F011229 BN45 Brassica napus cDNA clone BN45043006, mRNA
Bequence.
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Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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141: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'Genoplante' (http://www.genoplante.com

and http://genoplante.info.infoblogen.fr).
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Unpublished (2003)
Contact: Genoplante
Genoplante
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rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
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Contact: Genoplante
Genoplante
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Matches 134; Conservative 0; Mismatches 19; Indels 0;
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Search completed: May 18, 2004, 19:00:30 Job time : 1283.4 secs

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                            May 18, 2004, 19:02:23 ; Search time 2171 Seconds (without alignments) 998.227 Million cell updates/sec
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1 RLCERPSGTWSGVCGNNNAC......EHGSCNYVFPAHKCICYFPC 50
       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                 OM protein - nucleic search, using frame_plus_p2n model
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38: em htg.other: *
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AR014691 LOCUS LOCUS DEFINITION Sequence 14 from patent US 5773696. ACCESSION AR014691 AR014691 AR014691 AR014691 AR014691 AR014691 AR014691 AR014691 AR014691 GI:3972145 GENERAL ORGANISM Unknown. ORGANISM Unknown. ORGANISM Unknown. ORGANISM Unknown. ORGANISM Unknown. ORGANISM Unknown. AUTHORS Liang J., Shah, D.Maganlal., Wu, Y. Shun. and Rosenberger, C. Annette. TITLE Autifungal polypeptide and methods for controlling plant pathogenic fungi Location/Qualifiers SOURCE 1. 2.70 1. 2.70 HOLL YPPE="Unabsigned DNA"	Alignment Scores:	Argamicancysargamentuargalaciumisciysercysashryvalphepro Aggaccaargcagaaaccrrcaaaagacagaaccaarcrrccaacrargcrrccca AlaHislyscysilecystyrpheprocys 50	N W SE	JOURNAL Patent: US 6653280-A 14 25-NOV-2003; FEATURES Location/Qualifiers Source 1. 270 /organism="unknown" /mol_type="genomic DNA"	Alignment Scores: 3.38e-27

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1 (bases 1 to 285)
1 (bases 1 to 285)
Liang, J., Shah, D. Maganlal., Wu, Y. Shun. and Rosenberger, C. Annette.
Antifungal polypeptide and methods for controlling plant pathogenic
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1 (bases 1 to 500)

Liang, J., Shah, D.M., Wu, Y.S. and Rosenberger, C.A.

Antifungal polypeptide AlyAFP from Alyssum and methods for controlling plant pathogenic fungi

Patent: US 6653280-A 9 25-NOV-2003;

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/product="antifungal protein 1"
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Direct Submission
Submitted (14-DBC-1994) Franky R. Terras, F.A. Janssens Laboratory
of Genetics, Applied Biological Sciences, W. De Croylaan 42,
Heverlee, Belgium, B-3001
On Feb 9, 1995 this sequence version replaced gi:609321.
Location/Qualifiers
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/citation=[1]
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21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro
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                                                                                                                                                                                                                                                                                       Unclassified.

(Dases 1 to 285)

Liang, J., Shah, D.M., Wu, Y.S. and Rosenberger, C.A.

Antifungal polypeptide AlyAFP from Alyssum and methods for controlling plant pathogenic fungi
Patent: US 6652380-A 16 25-NOV-2003;

Location/Qualifiers
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Matches:
Conservative:
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Sequence 16 from patent US 6653280.
AR432392
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2 (bases 1 to 395)
Terras,F.R.
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AUTHORS TITLE

REFERENCE

224

Raphanus sativus (radish)

Raphanus sativus

REFERENCE AUTHORS

JOURNAL REFERENCE AUTHORS

TITLE

U18557.1 GI:644773

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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PAT 12-MAR-1998

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21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro
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Unclassified.
Unclassified.
Broekseart, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B., Terras, F.R.G. and Vanderleyden, J.
Biocidal proteins
Patent: US 5824869-A 48 20-OCT-1998;
                                                                                                                                                                                                                                                                      Broekaert, W.F., De, S.G., Rees and Sarah, B. ANTIFUNGAL PROTEINS
Patent: WO 9721814-A 19 19-JUN-1997;
ZENECA LID (GB)
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                                                                                      226 GCTCACAAGTGTATCTGCTACTTTCCTTGT 255
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/db_xref="taxon:32644"
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Sequence 19 from Patent WO9721814.
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/wol_type="unassigned DNA"
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A63404.1 GI:3717176
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; roside; eurosids II; Brassicales; Brassicaceae; Raphanus.
1 (bases 1 to 414)
Broekaert, W.F., Camue, B.P.A., Terras, F.R.G., Vanderleyden, J., Osborn, R.W. and Rees, S.B.
BIOCIDAL PROTEINS
PATENT: WO 3305153-A 33 18-MAR-1993;
ICI PLC (GB)
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/organism="Raphanus sativus"
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Location/Qualifiers
                                                                                                                                                /mol_type="unassigned DNA"
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Sequence 37 from Patent W09416076.
A39549
A39549.1 GI:2295842
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                                                                                                                                                                      21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
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                                                                                                                   Unclassified.

1 (bases 1 to 414)
Brockkert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B., Terras, F.R.G. and Vanderleyden, J.
Blockdal proteins
Patent: US 6187904-A 48 13-FBB-2001;
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Sequence 48 from patent US 5538525.
123728.1 GI:1603598
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I (bases 1 to 414)
Brockaert, W.F., Cammue, B.P.A., Osborn, R.W., Rees, S.B.,
Terras, F.R.G. and Vanderleyden, J.
Biocidal proteins
Patent: US 5538525-A 48 23-JUL-1996;
Location/Qualifiers
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Amplified Alyssum species antifungal polypeptide gene from pMON22652.
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/product= "AlyAFP antifungal polypeptide"
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/*tag= b
109. .258
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 27-MAR-1997;
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Aat99289 Alyssum s
Aat94581 Composite
Ad51221 Brassica
Aaq38650 Re-ARPI c
Aaq70128 Antimicro
Aat70333 Raphanus
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          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                       - nucleic search, using frame_plus_p2n model
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3: geneseqn2000s:*
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                                                                                                                                                                                                                                                                                                                                                                                                               geneseqn2004s:*
                                                                                                                                                                                                                       100%
                                                                                                                                                                                                                                                                                                                                                                                                                                     score greater than or equal to
and is derived by analysis of
                                                                                                                                                                                          length: 0
length: 2000000000
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Maximum Match 10
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                                                                                   US-10-681-972-2
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2286
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Match
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305
305
228
2283
283
283
                                                                                            Perfect score:
                                                                                                                 Scoring table:
                                                                                                                                                                            Total number
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Database

2 6 4 5 9 7 8

Result

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This sequence represents the cDNA sequence cloned into the E. coli cassette vector pMON2317 to generate vector pMON22652. The cDNA encodes the antifungal polypeptide AlyAFP, isolated from plants of the genus Alyssum. The AlyAFP polypeptide can be used to control phytopathogenic fungi, whilst the coding DNA can be used to produce transgenic plants that express the polypeptide making them resistant to the phytopathogenic fungi
                                                                                                                                                                                                                                                                                                                                                                                                       168
                                                                                                                                                                                                                                                                                                                                                                                                                                                    228
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                                                                                                                                                                                                                                                                                                                                                                                1 ArgleuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAsnAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                 109 AGGTTGTGCGAGAGAGCCAAGTGGGACATGGTCAGGAGTTTGTGGGAACAACAATGCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                           21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro
                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/product= "mature AlyAFP protein"
/note= "no start codon given at 5' end of sequence"
                                                                             Alyssum antifungal polypeptide and corresponding DNA - used in the production of transgenic plants resistant to phytopathogenic fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antifungal polypeptide; AlyAFP; inhibition; transgenic plant; phytopathogenic fungus; resistance; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alyssum species anti-fungal polypeptide AlyAFP cDNA sequence.
                                                                                                                                                                                                                                     270 BP; 75 A; 58 C; 60 G; 75 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                         270
50
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Matches:
Conservative:
Mismatches:
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                     Rosenberger CA;
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117. .269
                                                                                                                                                                                                                                                                                                                                                          x AAT94582 (1-270)
                                                                                                                   Example 4; Page 69; 92pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT94574 standard; cDNA; 286
                                                                                                                                                                                                                                                                           1.05e-26
                                                                                                                                                                                                                                                                                     305.00
100.00%
100.00%
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                       ₩u Y,
                                               WPI; 1997-503109/46.
(MONS ) MONSANTO CO.
                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                             US-10-681-972-2 (1-50)
                         Shah D,
                                                             P-PSDB; AAW35560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAY-1998
                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41
                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alyssum
                           Liang J,
                                                                                                                                                                                                                                                                                                                        Query Match:
DB:
                                                                                                                                                                                                                                                                               Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT94574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
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176
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                                                                                                                                    This sequence encodes the mature protein of an antifungal polypeptide (AlyAFP) isolated from plants of the genus Alyssum. The sequence was PCR amplified using primers AAT94583-194584, and the resultant 264 bp fragment was cloned as a BamHI fragment into the expression vector pMON2311 to generate plasmid pMON22652. The AlyAFP sequence in this plasmid is placed under control of an E355 promoter and the malze HSP70 intron I sequence. The protein can be used to control phytopathogenic fungi, whilst the DNA can be used to produce transgenic plants that express the protein making them resistant to the phytopathogenic fungi
                                                                                                                                                                                                                                                                                                                                                                                                         21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro
                                                                             Alyssum antifungal polypeptide and corresponding DNA - used in the production of transgenic plants resistant to phytopathogenic fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antifungal polypeptide; AlyAFP; inhibition; transgenic plant; phytopathogenic fungus; resistance; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "AlyAFP antifungal polypeptide"
                                                                                                                                                                                                                                                            Sequence 286 BP; 80 A; 62 C; 65 G; 79 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                  286
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AlaHisLysCysIleCysTyrPheProCys 50
                     Rosenberger CA;
                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alyssum species AlyAFP cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
53. .292
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                    US-10-681-972-2 (1-50) x AAT94574 (1-286)
                                                                                                                    Claim 12; Page 68; 92pp; English
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305.00
100.00%
100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a //product= '/product= '/*tag= b //*tag= b //*tag= c //*tag= c 439. .443
                      Wu Y,
                                              WPI; 1997-503109/46.
P-PSDB; AAW35558.
(MONS ) MONSANTO CO.
                                                                                                                                                                                                                                                                                                                                        Best Local Similarity:
                        Shah D,
                                                                                                                                                                                                                                                                                                                             Percent Similarity:
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                        ٦,
                                                                                                                                                                                                                                                                                                                                                     Query Match:
DB:
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WO9737024-A2

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                     140 AGGITGIGGGAGAGAGCAAGIGGGACAIGGIGGGAGTITGIGGGAACAACAAIGCAIGC 199
                                                                                                                                                                                                                                                                                                                           20
                                                                                                                                                                                                                                                                                                                                                            ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
                                                                                                                                                                                                                                                                                                                        1 ArgieuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys
                                                                                                                     Alyssum antifungal polypeptide and corresponding DNA - used in the production of transgenic plants resistant to phytopathogenic fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Composite cDNA sequence for Alyssum species antifungal polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antifungal polypeptide; AlyAFP; inhibition; transgenic plant; phytopathogenic fungus; resistance; ss.
                                                                                                                                                                                                                   Sequence 481 BP; 147 A; 88 C; 91 G; 154 T; 0 U; 1 Other;
                                                                                                                                                                                                                                             481
50
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                            Rosenberger CA;
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                                                                                                                                                                                                                                                                                                       US-10-681-972-2 (1-50) x AAT99289 (1-481)
                                                                                                                                               Example 4; Fig 1; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT94581 standard; DNA; 500 BP
                         97WO-US005709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-00627706,
                                          96US-00627706
                                                                                                                                                                                                                                           2.14e-26
305.00
100.00%
100.00%
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                                                                            Wu Y,
                                                                                           WPI; 1997-503109/46.
P-PSDB; AAW35560.
                                                                           Shah D,
                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MONS ) MONSANTO
                                                           (MONS ) MONSANTO
                                          29-MAR-1996;
                         27-MAR-1997;
                                                                                                                                                                                                                                    Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9737024-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAR-1997;
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       09-0CT-1997
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                                                                            Liang J,
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219 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 278
                                                                                                                                                                                                                                                                                                RACE (Rapid
                                                                                                                                                                                                                                     This sequence represents the cDNA sequence encoding the antifungal polypeptide AlyAFP, from plants of the genus Alyssum. The sequence represents a composite of the sequences isolated by 5' and 3' RACE (Rapic Amplification of cDNA Ends) methods (see AAT94577 and AAT94580). The AlyAFP polypeptide can be used to control phytopathogenic fungi, whilst the coding DNA can be used to produce transgenic plants that express the polypeptide making them resistant to the phytopathogenic fungi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ArgleucysgluargProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAsnAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro
                                                                                                       Alyssum antifungal polypeptide and corresponding DNA - used in the production of transgenic plants resistant to phytopathogenic fungi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .243
/*tag= a
/product= "Brassica oleracea defensin protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antimncropiai process; vectoris, pathogenic bacteria; composite disease resistance; pathogenic bacteria; rice white leaf blight; brown-stripe disease; glume blight; seedling damping-off disease; filamentous fungi; rice blight; lear blight; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 500 BP; 145 A; 89 C; 111 G; 154 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brassica oleracea defensin protein coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antimicrobial protein; defensin; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 AlaHisLysCysIleCysTyrPheProCys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels:
Rosenberger CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-681-972-2 (1-50) x AAT94581 (1-500)
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                                                                                                                                                                                   Example 4; Page 67; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-SEP-2001; 2001JP-00283117.
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296.00
98.00%
96.00%
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Wu Y
                                                     WPI; 1997-503109/46.
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Shah D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JP2003088379-A
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Liang J,
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91 AAGTTGTGCGAGAGGGGCCAAGTGGGACATGGTCAGAGGAGTCTGTGGAAACAATAACGCATGC 150
                                                              Novel protein from Brassica campestris, useful as antimicrobial against plant pathogenic filamentous fungi or pathogenic bacteria, especially for treating e.g. rice white leaf blight and sheath blight disease.
                                                                                                                                          The invention comprises the amino acid and coding sequences of antimicrobial (defensin) proteins from Brassica. The DNA and protein sequences of the invention are useful for producing transformed plants with composite disease resistance, especially resistant to diseases caused by pathogenic bacteria, such as: rice white leaf blight, brownstripe disease, glume blight, and seedling damping-off disease. As well as diseases, glume blight, and seedling damping-off disease. As well sed disease, and leaf blight. The present DNA sequence encodes a Brassica defensin protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ArgleuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria; fungloide; bacteriocide; antibiotic; antifungal; gram positive; plant disease resistance; low toxicity.
                                                                                                                                                                                                                                                                                         G; 125 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                   394
200
300
300
300
                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 GCTCACAAGTGTATTTGCTACTTCCCTTGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaHisLysCysIleCysTyrPheProCys 50
                                                                                                                                                                                                                                                                                                                                                                                            Indels:
Gaps:
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16. .256
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-681-972-2 (1-50) x ADC51221 (1-394)
                                                                                                                             Claim 3; SEQ ID NO 1; 34pp; Japanese
                                                                                                                                                                                                                                                                                            Sequence 394 BP; 116 A; 71 C; 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ38650 standard; DNA; 414 BP
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283.00
96.00%
90.00%
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                              WPI; 2003-621123/59.
P-PSDB; ADC51222.
                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ38650;
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
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                                                                                                                                                                                                                                                                                                                                                            Score:
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This cDNA represents the sequence of Rs-AFPI from Raphanus sativus. PCR primer AAQ38640 was used together with AAQ38641 to generate a probe for primer AAQ38640 was used together with AAQ38641 to generate a probe for screening a Raphanus sativus seed cDNA library. This primer corresponds to amino acids 2 to 7 of Rs-AFPI and has a sense orientation. The 144bp coduct was partially re-amplified using AAQ38642 and AAQ38641 to give a class product, which was further reamplified with the same primers and class product. This was used to screen a lambda ZAPII cDNA library by in situ product. This was used to screen a lambda ZAPII cDNA library by in situ conflictional screening rounds with the same probe. Inserts were excised in vivo into the pBluescript phagemid form with the aid of helper phage to two additional screening rounds with the same probe. Inserts were excised in their size compared by agarose gel electrophoresis. Four clones had their size of approx. 400bp the others between 250-300bp. The inserts of the 4 largest clones were then sequenced and found to differ only in the length of their s' and 3' UTR's. The longest sequence is given here.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antimicrobial; Rs-AFP1; symbiosis; disease-resistance; fungus-resistance; Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40
                                                                                                                                                                   Biocidal proteins isolated from seeds of plants - e.g. brassica or dahlia, useful for increasing plants' resistance to fungal and bacterial diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 ArgasndincysargasnLeugluargalagluHisGlySerCysasnTyrValPhePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ArgleuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 pagrigieceanadeccandreeacaregreacagraricrererannacarinacearec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Terras FRG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 414
45
                                                                                    Rees SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 GCTCACAAGTGTATCTGCTACTTTCCTTGT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 AlaHisLysCysIleCysTyrPheProCys
                                                                                    Cammue BPA, Osborn RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-681-972-2 (1-50) x AAQ38650 (1-414)
                                                                                                                                                                                                                                                  Example 21; Fig 35; 110pp; English.
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                                                    (ICIL ) IMPERIAL CHEM IND PLC
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283.00
96.00%
90.00%
92GB-00003038.
92GB-00013526.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antimicrobial Rs-AFP1
                                                                                                                                          WPI; 1993-100978/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
                                                                                                          Vanderleyden J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
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                                                                                          Broekaert WF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
   13-FEB-1992;
25-JUN-1992;
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DB:
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IID AAQ7
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Raphanus sativus

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AAT68696 standard; cDNA; 414 BP
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                                                                                             96WO-GB003068.
                                                                                                                95GB-00025455.
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96.00%
90.00%
92.79%
.102
ag= b
                  .255
           /*tag=
                              /*tag=
                                                                                                                                                                                                                                                                         Claim 8; Fig 2; 65pp;
                  103.
                                                                                                                                                                                                       WPI; 1997-332786/30.
                                                                                                                                               (ZENE ) ZENECA LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
                                                                                                                                                                 Puijk
                                                                                                                                                                                                                 P-PSDB; AAW19280.
                                                                                                                                                                                   Van Gelder WMJ;
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                                                                                                                                                                           Broekaert W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                               12-DEC-1996;
                                                                                                                   13-DEC-1995;
                                                                                                                             28-MAR-1996;
                                                          WO9721815-A2
                                                                             19-JUN-1997
 sig_peptide
                   mat_peptide
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DB:
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ID AAT6
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                            165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antifungal protein; candida; fungal resistance; food additive; radish; crop protection; plant defensin; bacterial protection; preservative; ss.
                                                                                                                                                                                                                 plant-derived antimicrobial proteins are expressed in endosymbiotic clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with recombinant Cxc are protected against fungal disease. A suitable antimicrobial protein is Rs-AFPl from R. sativus. The full-length cDNA sequence of Rs-AFPl is given in AAQ70128. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                       1 ArgleuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
                                                                                                                                                          Antimicrobial protein producing endo-symbiotic microorganisms - is produced by combining nucleic acids encoding the protein with an endophyte, useful for protecting plant hosts from esp. fungal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                          106 AAGTIGIGCGAAAAGGCCAAGTGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC
                                                                                                                                                                                                                                                                                      Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/transl except= (pos:85. .87, aa:Glu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Raphanus sativus antifungal protein I (Rs-AFPI) cDNA.
                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AlaHisLysCysileCysTyrPheProCys 50
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                                                                                                                                                                                                                                                                                                                                                                                       x AAQ70128 (1-414)
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                                                                                                                                                                                                    Disclosure; Page 31; 39pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT72333 standard; cDNA; 414 BP
                                                                                                               SB;
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283.00
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                                                                                                                Powell KA,
                                                                                                                                   WPI; 1994-249223/30.
                                                                                             (ZENE ) ZENECA LID
                                                                                                                                                                                                                                                                        correct PN field.)
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Best Local Similarity:
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                                                                                                                                              P-PSDB; AAR57325
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Pred. No.:
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                                                       05-JAN-1994;
                                                                           08-JAN-1993;
                  WO9416076-A1
                                                                                                                  Dubock AC,
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Antifungal peptide derived from radish antifungal protein 2 - and related DNA, useful for producing plants with increased fungal resistance and as therapeutic or preservative agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sijtsma L, Van Amerong
Borremans FAM, Rees SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
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Mismatches:
/product= "antifungal_protein_1"
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Samblanx GW, Fant F,
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BP.

standard; DNA; 426

ADC51223

(first entry)

18-DEC-2003

.87, aa:Glu)

(pos:85.

16. 258 /*tag= a /transl_except= (16. 102

/*tag= b 103. .255 /*tag= c

Location/Qualifiers 16. .258

ADC51223; ADC51223

(first entry)

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This cDNA clone codes for the preprotein for radish antifungal protein I (Rs-AFP1) (AAW19617). Novel antifungal proteins are based on Rs-AFP1, Rs-AFP2 (see AAW19616), Rs-AFP3 and Rs-AFP4, especially those in which Gly9 is repaced by Arg, Val39 by Arg, Gly9 by Arg, Glu5 by Met and/or Gly6 by Met. Mutants (see AAW26371-90) of Rs-AFP2 are specifically claimed. The mutants show improved salt tolerant antifungal activity, particularly
                                                                                                                                                                                                                                                                                                                                                                                                                                                       New active mutants of radish antifungal protein 2 - used to gener fungus-resistant plants or as therapeutic or preservative agents.
                                                                      Rs-AFP1; radish antifungal protein 1; fungicide; salt tolerance; preservative; transgenic plant; crop protection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 414 BP; 128 A; 74 C; 80 G; 132 T; 0 U; 0 Other;
                                                 Radish antifungal protein 1 (Rs-AFP1) cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       when expressed in plants
                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-332785/30.
                                                                                                                                                                                                                                                                                                                                                                 (ZENE ) ZENECA LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAW19617
                                                                                                                  Raphanus sativus
                                                                                                                                                                                                                                                                                                                                                                                            Broekaert WF,
                                                                                                                                                                                                                                                                                                                 12-DEC-1996;
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                        13-DEC-1997
                                                                                                                                                                                               sig_peptide
                                                                                                                                                                                                                      mat_peptide
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Query Match
                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score:
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SB; Rees

De Samblanx GW,

96WO-GB003065 95GB-00025474

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Novel protein from Brassica campestris, useful as antimicrobial against plant pathogenic filamentous fungi or pathogenic bacteria, especially for treating e.g. rice white leaf blight and sheath blight disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention comprises the amino acid and coding sequences of antimicrobial (defensin) proteins from Brassica. The DNA and protein sequences of the invention are useful for producing transformed plants with composite disease resistance, especially resistant to diseases caused by pathogenic bacteria, such as: rice white leaf blight, brownstripe disease, glume blight, and seedling damping-off disease. As well as diseases caused by filamentous fungi, such as: rice blight, sheath blight disease, and leaf blight. The present DNA sequence encodes a Brassica defensin protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 AAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ArgleuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 AAGTTGTGCGAGAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC
                                                                                                                         composite disease resistance; pathogenic bacteria; rice white leaf blight; brown-stripe disease; glume blight; seedling damping-off disease; filamentous fungi; rice blight; sheath blight disease; leaf blight; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 426 BP; 142 A; 72 C; 84 G; 128 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                      /*tag= a
/product= "Brassica defensin protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44600
22
3
                                                                                                          protein; defensin; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                           (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
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                                                                              Brassica defensin protein coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 AlaHisLysCysIleCysTyrPheProCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; SEQ ID NO 3; 34pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (1-426)
                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-681-972-2 (1-50) x ADC51223
                                                                                                                                                                                                                                                                                                                                                                                                               18-SEP-2001; 2001JP-00283117.
                                                                                                                                                                                                                                                                                                                                                                                 18-SEP-2001; 2001JP-00283117
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283.00
96.00%
90.00%
                                                                                                                                                                                                                                                       .243
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P-PSDB; ADC51224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity:
                                                                                                                                                                                                                                                                                                                     JP2003088379-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                          gb.
                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
                                                                                                                                                                                                         Brassica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local
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used to generate

150

20

165

Length:
Matches:
Conservative:
Mismatches:
Indels:

46e-24 283.00 96.00% 90.00% US-10-681-972-2 (1-50) x AAT68696 (1-414)

106 AAGTIGIGCGAAAGGCCAAGIGGGACAIGGICAGGAGICIGIGGAAACAAIAACGCAIGC ArgleuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys

991 41 226

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AlaHisLysCysIleCysTyrPheProCys 50

RESULT 10

210

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Protecting plants against pathogens by inducing defensin genes - by stimulating ethylene or jasmonate pathways, also new promoter of defensin gene from Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence encodes the Arabidopsis PDF1.1 gene which is used in a novel method for the protection of plants against pathogens which involves inducing expression of a plant defensin gene by stimulating the jasmonate and/or ethylene pathways. The method is used to induce protection against necrotrophic pathogens, specifically fungi and does not require cytotoxic or potentially harmful chemicals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 AAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ArgieuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro
                                                                                                                          Defensin; PDF1.1; protection; plant; pathogen; jasmonate; ethylene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Terras FRG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 403 BP; 112 A; 77 C; 85 G; 129 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Penninckx IAMA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
                                                                                                                                                                                                                                                                                  /product= "PDF1.1"
/note= "plant defensin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-681-972-2 (1-50) x AAV10632 (1-403)
                                                                                                                                                                                         Location/Qualifiers
26. .268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig 1, 72pp, English.
                       BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thomma BPHJ,
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                       AAV10632 standard; DNA; 403
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96.00%
88.00%
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114..265
                                                                       (first entry)
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                                                                                                                                                                                                                               113
                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                       /*tag=
                                                                                                 PDF1.1 DNA
                                                                                                                                                                 Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-086663/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAW40345.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Broekaert WF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1996;
                                                                                                                                                                                                                                                                                                                         WO9800023-A2
                                                                                                                                                                                                                                                                                                                                                                           20-JUN-1997;
                                                                                                                                                                                                                                 sig_peptide
                                                                                                                                                                                                                                                                                                                                                   08-JAN-1998
                                                                         23-JUN-1998
                                                                                                   A. thaliana
                                                                                                                                                                                                                                                           mat_peptide
                                                                                                                                          fungi; ss
                                               AAV10632,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kazan K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
         AAV10632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance to tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210
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                                                                                                                                                                                                                                                                                                                                                                                                     Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ArgleuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro
                                                                                                                                                      Plant; bacterial infection; fungal infection; viral infection; ds.
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                                                                                                                                                                                                                                                                                                                                        Zon
                                                                                                                                                                                                                                                                                                                                       Hon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 243 BP; 58 A; 56 C; 59 G; 70 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2444000
844
                                                                                                                                                                                                                                                                                                                                        Glazebrook J, Goff
Whitham S, Xie Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
GCTCACAAGTGTATTTGCTACTTCCCTTGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AlaHisLysCysIleCysTyrPheProCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; SEQ ID NO 747; 899pp; English.
                                                                                                                               SEQ ID 747.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-681-972-2 (1-50) x ADA68378 (1-243)
                                                                                                                                                                                                                                                                                                           (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                    BP
                                                                                                                                                                                                                                                                                                                                        Cooper B,
S, Tao Y,
                                                                                                                                                                                                                                                                                      22-JUN-2001; 2001WO-IB001105
                                                                                                                                                                                                                                                             22-JUN-2001; 2001WO-IB001105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28e-23
                                                   ADA68378 standard; DNA; 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             278.00
96.00%
88.00%
91.15%
                                                                                                                                Arabidopsis thaliana gene,
                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention.
                                                                                                                                                                                                                                                                                                                                                    Katagiri F, Quan S,
                                                                                                                                                                                 Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-175290/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                         Chen W,
                                                                                                                                                                                                            WO2003000898-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     illustrate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                       20-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41
                                                                              ADA68378;
                                                                                                                                                                                                                                                                                                                                           Chang H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                             RESULT 11
                                           ADA68378
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Manners

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Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria; fungicide; bacteriocide; antibiotic; antifungal; gram positive; plant disease resistance; low toxicity.
                                                                                                                                                                                                                         Cammue BPA, Osborn RW, Rees SB,
Location/Qualifiers
16. .256
/*tag= a
                                                                                                                                                                                       91GB-00018523.
92GB-00003038.
92GB-00013526.
                                                                                                                                                                                                              (ICIL ) IMPERIAL CHEM IND PLC
                                                                                                                                                                           92WO-GB001570.
                                   AAQ38652 standard; DNA; 261
                                                           (revised)
(first entry)
                                                                                                                                                                                                                                           WPI; 1993-100978/12.
                                                                                                                 Raphanus sativus.
                                                                                                                                                                                                                          Broekaert WF, 'Vanderleyden J;
                                                                                                                                                                                       29-AUG-1991;
13-FEB-1992;
                                                                                                                                                                           27-AUG-1992;
                                                                                                                                                                                                   25-JUN-1992;
                                                                              RB-AFP2 CDNA
                                                                                                                                                     W09305153-A1
                                                            25-MAR-2003
07-JUL-1993
                                                                                                                                                                18-MAR-1993
                                                                                                                                                                                                                                                                    diseases.
                                                AAQ38652;
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Biocidal proteins isolated from seeds of plants - e.g. brassica or dahlia, useful for increasing plants' resistance to fungal and bacterial

Terras FRG;

Example 21; Fig 35; 110pp; English.

This cDNA represents the sequence of Rs-AFP2 from Raphanus sativus. PCR primer AAQ38640 was used together with AAQ38641 to generate a probe for primer AAQ38640 was used together with AAQ38641 to generate a probe for screening a Raphanus sativus seed cDNA library. This primer corresponds to amino acids 2 to 7 of Rs-AFP1 and has sense orientation. The 144bp product was partially re-amplified using AAQ38642 and AAQ38641 to give a clagoxigenin-11-dUTP instead of dTTP to give a digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR product. This was used to screen a lambda ZAPII cDNA library by in situ product. This was used to screen a lambda ZAPII cDNA library by in situ plaque hybridisation. Positive plaques were purified and subjected to two plaque hybridisation promise with the same probe. Inserts were excised in vivo into the pBluescript phagemid form with the aid of helper phage crimers is zec compared by agazose gel electrophoresis. Four clones had contained to their states of approx. 400bp the orthers between 250-300b; The inserts of the largest clones were then sequenced and found to differ only in the langest sequence was identified as Rs-AFP1 so the Rs-AFP2 was seen to differ by only 2 amino acids from Rs-AFP1, so the Rs-AFP2 was seen to differ by only 2 amino acids from Rs-AFP1, so the Rs-AFP2 was sasisted site directed mutagenesis. (Updated 25-MAR-2003 to correct PN field.)

Sequence 261 BP; 67 A; 55 C; 59 G; 80 T; 0 U; 0 Other;

Alignment Scores:

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Plant-derived antimicrobial proteins are expressed in endosymbiotic clavibacter xyli subsp. cynodontis (Cxc). Plants or seeds treated with recombinant Cxc are protected against fungal disease. A suitable antimicrobial protein is Rs-AFPI from R. sativus. The full-length cDNA sequence of PCR assisted site-directed mutagenesis of Rs-AFP2 is given in AAQ70130 and the deduced amino acid sequence in AAR57327. (Updated on 25-
                                                                                                                                                                                                                                                                                                                                                                                                                         Antimicrobial; Rs-APP2; symbiosis; disease-resistance; fungus-resistance; Clavibacter xyli subsp. cynodontis; Cxc; crop improvement; endophyte; PCR; polymerase chain reaction; mutagenesis; ss.
                                                                                                                                                                                         21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antimicrobial protein producing endo-symbiotic microorganisms - is produced by combining nucleic acids encoding the protein with an endophyte, useful for protecting plant hosts from esp. fungal disease.
                                                                                                                     1 ArgleuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
                                                                                                                                   G; 83 T; 0 U; 0 Other
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Matches:
Conservative:
 Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                           GCTCACAAGTGTATCTGCTACTTTCCTTGT 255
                                                     Indels:
                                                                                                                                                                                                                              41 AlaHisLysCysIleCysTyrPheProCys
                                                                   Gaps:
                                                                                            US-10-681-972-2 (1-50) x AAQ38652 (1-261)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 33; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 A; 66 C; 69
                                                                                                                                                                                                                                                                                                          BP.
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274.00
94.00%
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    4.08e-23
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               274.00
94.00%
86.00%
89.84%
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                                                                                                                                                                                                                                                                                                                                                                (revised)
                                                                                                                                                                                                                                                                                                                                                                                                    Antimicrobial Rs-AFP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1994-249223/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ZENE ) ZENECA LTD
                           Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Raphanus sativus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAR57327
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
14-FEB-1995
                                                                                                                                                                                                                                                                                                                                      AAQ70130;
                                                        Query Match:
     Pred. No.:
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Mismatches:

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Search completed: May 18, 2004, 20:38:40 Job time : 300 secs
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                                                                                 Raphanus sativus antibacterial protein radishin encoding DNA SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated DNA from Raphanus sativus used to transform a microbe and a plant to produce an antibacterial protein used to increase resistance of rice paddy against pathogenic microbes.
                                                                                                                1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAshAlaCys 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence encodes an antibacterial protein, designated radishin, isolated from Raphanus sativus (radish). A phage or plasmid comprising radishin can be used for increasing resistance of paddy and rice blast disease against pathogenic microbes
                                                                                                                                                                                                                                                                                                                          Raphanus sativus; antibacterial; plant; resistance; paddy; radishin; pathogenic microbe; radish; rice blast disease; ds.
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Indels:
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                                              US-10-681-972-2 (1-50) x AAQ70130 (1-288)
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P-PSDB; AAY91117.
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Best Local Similarity:
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Query Match:
DB:
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191 AAGAATCAGTGCATTCGACTTGAGAAAGCACGACGACGTGGGTCTTGCAACTATGTCTTCCCA 250
21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro
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APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Youn's Sond Mericant Roseberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 5773696th
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
CPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
US-08-377-687-48
US-08-771-192-48
US-08-971-982-48
US-09-077-951-19
US-09-077-951-19
US-09-077-948A-45
US-08-103-489-17
US-08-277-06-17
US-08-777-192-58
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US-09-103-489-8
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US-08-971-982-36
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US-08-377-687-34
US-08-777-192-34
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TELEPHONE: (314) 537-6224
                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-627-706-14; Sequence 14, Application US/08627706; Patent No. 5773696; GBNERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 436
ATTORNEY/AGRAT INFORMATION:
NAME: COhen, Charles E.
REGISTRATION NUMBER: 34,565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 14:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy 0
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-Q-GOR2_1/USPTO_spool/US10681972/runat_17052004_151740_4379/app_guery.fasta_1.199
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-NO MAAD- LARGEQUERY -NRGS_CORES=0 -WAIT -DSPELOCK=100 -LONGLOG
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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12, Appl
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440.437 Million cell updates/sec
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1 RLCERPSGTWSGVCGNNNAC.....BHGSCNYVFPAHKCICYFPC
                                                                                             May 18, 2004, 20:26:28 ; Search time 63 Seconds
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6: /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                       - nucleic search, using frame_plus_p2n model
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US-09-103-489-14
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Maximum Match 100%
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APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: CONTROLLING Plant Pathogenic Fungi NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS: 20
CORRESPONDENCE ADDRESS: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 6215048th
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER: IBA PC Compatible
COMPUTER: IBA PC Compatible
COMPUTER: IBA PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-UN-1998
CLASSIFICATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700) A
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION POR SEQ ID NO: 14:
TEMERAX: (314) 537-624
TELECOMMUNICATION POR SEQ ID NO: 14:
TEMERAX: (314) 5-77-604
TEMERAX: (314) 5-77-604
                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
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US-09-103-489-14
'Sequence 14, Application US/09103489
'Patent No. 6215048
                                                                                                                                                                          9.41e-31
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SEQUENCE CHARACTERISTICS:

LENGTH: 270 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLIGY: linear

MOLECULE TYPE: cDNA
US-08-627-706-14
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Query Match:
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Matches:
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                                                                                                                                                          41 AlaHisLysCysIleCysTyrPheProCys 50
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ORGANISM: Artificial Sequence
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COTHER INFORMATION: Plasmid
US-09-829-381D-14
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Best Local Similarity:
Query Match:
                  Percent Similarity:
Best Local Similarity:
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Patent No. 663230
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Rescherger, Cindy A.
TILLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control
TILLE OF INVENTION: Plant Pathogenic Fungi
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICANTION NUMBER: US/09/829,381D
CURRENT FILING DATE: 2001-04-09
PRIOR FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
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TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCE: 20 CORRESPONDENCE ADDRESS: ADDRESSE: Charles E. Cohen, Monsanto Company, BB4F STREET: 700 Chesterfield Village Parkway No. 6215048th CITY: St. Louis STATE: Missouri
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPANIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/103,489
FILLING DATE: US/09/103,489
FILLING DATE: US/09/103,489
FILLING DATE: US/09/103,489
FILLING NUMBER: 34,565
REGISTRATION: 800
MATONREY/AGART IRFORMATION:
NAME: COCHEN, Charles E:
REGISTRATION NUMBER: 34,565
REGISTRATION NUMBER: 34,565
REJERRENCE/DOCKET NUMBER: 34,565
REJERRENCE/DOCKET NUMBER: 34,565
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Matches:
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity:
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US-09-103-489-12
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DB:
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                                                                                              APPLICANT: Ling, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. 5773696th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
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US-09-103-489-12

Sequence 12, Application US/09103489

Patent No. 6215048

GENERAL INFORMATION:

APPLICANT: Liang, Jihong

APPLICANT: Shah, Dilip M.

APPLICANT: Rosenberger, Cindy A.
   Sequence 12, Application US/08627706
Patent No. 5773696
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION UNDRER: 34,565
REFERENCE/DOCKET 134,565
REPERENCE/DOCKET 136,237
TELECOMMUNICATION INFORMATION:
TELEPAK: (314)537-624
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.02e-30
305.00
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 436
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STATE: Missouri
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98.00#
96.00#
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                  Best Local Similarity:
; MOLECULE TYPE:
US-08-627-706-9
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                                                         Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/08627706

| Sequence 9, Application US/08627706
| Patent No. 5773696
| GENERAL INFORMATION:
| APPLICANT: Liang, Jihong
| APPLICANT: Bhah, Dilip M.
| APPLICANT: Ru, Yonnie S.
| APPLICANT: Ru, Yonnie S.
| APPLICANT: Ru, Yonnie S.
| APPLICANT: Ru, Yonnie S.
| TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
| TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
| TITLE OF ADDRESSE: Charles E. Cohen, Monsanto Company, BB4F
| ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Charles E. Cohen, Monsanto Company, BB4F 700 Chesterfield Village Parkway No. 5773696th
                                                                                                                                                                                                             286
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,706
                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                      ; OTHER INFORMATION: Synthetic PCR reaction product US-09-829-381D-12
                                                                                                                                                                                                                                                                                                                                              US-10-681-972-2 (1-50) x US-09-829-381D-12 (1-286)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles B.
REGISTRATION NUMBER: 34,565
REPERENCE/DOCKET NUMBER: 38-21 (10700) A
TELECOMMINICATION:
TELECOMMINICATION:
TELEPHONE: (314)537-624
TELEPRAX: (314)537-6047
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TELEPHONE: (314,727-6047
TELEPHONE: (314)537-6047
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH: 500 base pairs
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                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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305.00
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     NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 12
LENGTH: 286
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CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
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Alignment Scores:

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Conservative:

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21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro
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APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods for TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
                                                                                                                                                    3: Charles B. Cohen, Monsanto Company, BB4F 700 Chesterfield Village Parkway No. 5773696th
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Wu, Yonnie S.
APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: Antifungal Polypeptide and Methods J
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
NUMBER OF SEQUENCES: 19
CORRESPONDEMES: 19
CORRESPONDEMES: Charles E. Cohen, Monsanto Company, BB4F
                                                                                                                                                                                                                                     COUNTEX: USAN

ZIP: 63198

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NAMER: US/08/627,706
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E:
REFERENCES/DOCKET NUMBER: 38-21(10700)A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 16:
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3 4 5
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16, Application US/09103489
Patent No. 6215048
GENERAL INFORMATION:
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283.00
96.00%
90.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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Best Local Similarity:
                                                                                                                                                                          STREET: 700 Cher
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
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                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
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Patent No. 6653280

GENERAL INFORMATION:
APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Plant Pathogenic Fungi
TITLE OF INVENTION: Plant Pathogenic Fungi
TITLE REFERENCE: 38-21 (10700) C
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR PILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 500
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                                                                                                                                                        159 AAGTICICILIA 1100 AAGTICIAAGICGAACAIGGICAGGCGIGIGIGIGGGAATAAIAAGGCAAGG 218
                                                                                                                                                                                                                   219 AGGAACCAATGCAGAAACCTTGAAAGAGAGAGAACAGGATCTTGCAATGTGTCTTCCCA 278
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48
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Matches:
Conservative:
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Indels:
Gaps:
           Mismatches:
Indels:
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                                                                                  US-10-681-972-2 (1-50) x US-09-103-489-9 (1-500)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (22)...(22)
; THER INFORMATION: N = any nucleotide
US-09-829-381D-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-627-706-16; Sequence 16, Application US/08627706; Patent No. 5773696; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.05e-29
296.00
98.00%
96.00%
           96.00%
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ORGANISM: Alyssum spp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
Query Match:
           Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                 Query Match:
DB:
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21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
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                                                                                                                                                                                                                              ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16,773
R: 99042/SEE.36525/US/A
                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
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Indels:
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Facent No. 5538525
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: TERRA, FRARH B.
APPLICANT: TERRA, FRANKX R.G.
APPLICANT: TERRAS, FRANKX R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
TITLE OF INVENTION: BIOCIDAL PROTEINS
CORRESPONDENCE ADDRESS:
ADDRESSE: CUSHMAN DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
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CLASSIPICATION: 800
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTONNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.3
TELEPHONE: 202-861-3000
                                                                      TYPE: DNA
ORGANISM: Artificial Seguence
FEATURE:
  SOFTWARE: Patentin version 3.1
                                                                                                                                       ; OTHER INFORMATION: Synthetic US-09-829-381D-16
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96.00%
90.00%
92.79%
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs
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Best Local Similarity:
Query Match:
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Pred. No.:
                        SEQ ID NO 16
LENGTH: 285
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APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: W. Younle S.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Contro
TITLE OF INVENTION: Alant Parthogenic Fungi
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/09/829,381D
CURRENT FILING DATE: 2001-04-09
PRIOR PAPLICATION NUMBER: 09/103,489
RAICR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
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NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Cheeterfield Village Parkway No. 6215048th
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                     COMPUTER READABLE FURM:
MEDITUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURSENT APPLICATION DATA:
APPLICATION NUMBER: US/09/103,489
FILING DATE: 24-JUN-1998
CLLASSIFICATION: 800
ATTORNEY AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/POCKET NUMBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEBRONE: 3314) 537-6047
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 Dasse pairs
TYPE: nucleic acid
TYPE: nucleic acid
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45
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Matches:
Conservative:
Mismatches:
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MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16, Application US/09829381D Patent No. 6653280 GENERAL INFORMATION:
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96.00%
90.00%
92.79%
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity:
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166 AAGAATCAGTGCATTAACCTTGAGAAAGCACGACGAGGATCTTGCAACTATGTCTTCCCA 225
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Comparible
COMPUTER: IBM FO COMPATIBLE
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/971,982
FILING DATE: 17-NO. 6187904-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-408-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL. N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                              US-10-681-972-2 (1-50) x US-08-777-192-48 (1-414)
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TERRAS, FRANKY R.G.
VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BROEKAERT, WILLEM F. CAMMUE, BRUNO P.A. OSBORN, RUPERT W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
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283.00
96.00%
90.00%
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ZIP: 20005
TYPE: nucleic acid
STRANDEDNESS: both
             STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
                                                                      ; FEATURE:
; NAME/KEY:
; LOCATION:
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Pred. No.:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,192
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Mismatches:
Indels:
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REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
                                                                                                                                                                                                                                                                                                            US-10-681-972-2 (1-50) x US-08-377-687-48 (1-414)
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                                                                                                                                                                                   Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BROEKAERT, WILLEM F.
APPLICANT: CAMMUB, BRUNO P.A.
APPLICANT: OSBORN, RUBERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-GAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 48, Application US/08777192
Patent No. 5824869
GENERAL INFORMATION:
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TELEPHONE: 202-861-3000
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283.00
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90.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 TYPE: nucleic acid
STRANDEDNESS: both
                                                     MOLECULE TYPE: CDNA FEATURE:
                                                                                           ; NAME/KEY: CDS
; LOCATION: 16..255
US-08-377-687-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: WASHINGTON
                                        linear
                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: D.C.
                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-08-777-192-48
                                          TOPOLOGY:
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                                                                                                                                                                                       Pred. No.:
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Length:
Matches:
Conservative:
Mismatches:
Indels:
                                     NAME/KEY: CDS
LOCATION: 16..255
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-08-971-982-48
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
                                                                                                      1.1e-27
283.00
96.00%
90.00%
                                                                                              Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Percent Local Similarity:
Query Match:
3
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Search completed: May 18, 2004, 21:56:21 Job time : 64 secs

US-10-681-972-2 (1-50) x US-08-971-982-48 (1-414)

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2, Appl Appli , Appli , Appl

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Sequence 48, Appl
Sequence 45, Appl
Sequence 13, Appl
Sequence 17, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 2046, Ap
Sequence 2046, Ap
Sequence 15, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 283, App
Sequence 34, Appl
Sequence 36, Appl
Sequence 29, Appli
Sequence 31, Appli
Sequence 31, Appli
Sequence 31, Appli
Sequence 48, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Appl
Sequence 21, Appl
Sequence 3, Appli
Sequence 17, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
                                  Sequence 12, Appl
Sequence 12, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 31,
Sequence 31, 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15,
                                                                                                               Sequence 16,
                                                                                    Seguence 9,
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                                                                                                   Sequence 16,
                                                                  Sequence 9,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods:
Controlling Plant Pathogenic Fungi
US-09-829-381A-14
3 US-10-681-972-14
3 US-10-681-972-14
3 US-10-681-972-12
3 US-10-681-972-12
3 US-10-681-972-13
3 US-10-681-972-9
3 US-10-681-972-9
3 US-10-681-972-16
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4 US-09-759-584-58
4 US-10-973-561-13
3 US-10-973-981-972-9
1 US-09-938-842A-2046
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5 US-10-178-449A-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/09829381A Patent No. US20020144306A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                 373
156
250
610
658
579
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1150
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464
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1616
306
306
284
   US-09-829-381A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
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-MODEL=frame+ p2n.model -DEV=xlh
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-DE=Published Applications NA -OFMT=fastap -SUFFIX=p2n.Tnpb -MINMATCH=0.1
-LOOPCIL=0 -LOOPERT=0 -UNITS=bits -START=1 - BND=-1 -MATRIX-Ebitsum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTPMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXIEN=200000000 -USER=USI0681972 @CGN I 1 164 @rumat 17052004 151741 4466
-NCPU-6 -ICPU-3 -NO MAAP -LARGEQUERT -NEG SCORES=0 -WAIT -DSPBLOCR=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -SGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                     May 18, 2004, 21:15:19; Search time 289 Seconds (without alignments) 785.130 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                         305
1 RLCERPSGTWSGVCGNNNAC......EHGSCNYVFPAHKCICYFPC 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications NA:*

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2: /cgn2_6/ptodata/1/pubpna/USOT_NEW_PUB.seq:*
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19: /cgn2_6/ptodata/1/pubpna/USOE_PUBCOMB.seq:*
        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                        nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                        2947324 seqs, 2269024515 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

Length DB

Query Match

Score

length: 0 length: 2000000000

Minimum DB seq Maximum DB seq

Searched:

0.5

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

BLOSUM62

Scoring table:

US-10-681-972-2

Perfect score:

Sequence:

OM protein

Run on:

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169 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTTTCCCA 228
                                                                                                                                                                                                                                                                                                             40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: Charles E. Cohen, Monsanto Company, BB4F
STREET 700 Chesterfield Village Parkway No. US20020144306Alth
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                109 AGGTTGTGCGAGAGCCAAGTGGGACATGGTCAGGAGTTTGTGGGGAACAACAATGCTGC
                                                                                                                                                                                                                                 1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys
                                                                                                                                                                                                                                                                                                               21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGULT: 3
US-09-29-381A-12
Sequence 12, Application US/09829381A
Sequence 12, Application US/09829381A
Fatent No. US20020144306A1
Sequence 12, Application US/09829381A
GENERAL INFORMATION:
Washap, Jihong
Napplication Not Shah, Jihong
Rosenberger, Cindy A.
TITLE OF INVENTION: Anticungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version #1.30
                                                     270
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                                                       Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-681-972-2 (1-50) x US-10-681-972-14 (1-270)
                                                                                                                                                                                                                                                                                                                                                                                         41 AlaHisLysCysIleCysTyrPheProCys 50
                                                                                                                                     Indels:
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US-09-829-381A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-6047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 286 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                           305.00
100.00%
100.00%
                                                                                      Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aliqnment Scores:
                                    Alignment Scores:
Pred. No.:
  US-10-681-972-14
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APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control TITLE OF INVENTION: Plant Pathogenic Fungi
FILE REPERENCE: 38-21 (10700) C.
CURRENT PAPLICATION NUMBER: US/10/681,972
CURRENT PAPLICATION NUMBER: US/09/829,381D
PRIOR FILING DATE: 2001-04-09
PRIOR PELICATION NUMBER: 09/103,489
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
LENGTH: 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 addrifordonanaczangradancardercadangrifordonancancardardera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 AGGAACCAATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ArgleuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  270
0
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-681-972-2 (1-50) x US-09-829-381A-14 (1-270)
                                                                                                                                                                                                                                   TELECOMMUNICATION INPORMATION:
TELEPRA: (314) 537-624
TELEPRA: (314) 537-6047
INPORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
TYPE: moleic acid
STRANDEDNESS: single
DOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 derekakardrárrigirácirecekrer 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 AlaHisLysCysIleCysTyrPheProCys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 14, Application US/10681972; Publication No. US20040064850A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.27e-33
305.00
100.00%
100.00%
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OTHER INFORMATION: Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-829-381A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
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21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
                                                                                                                                                               NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ArgleuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219 AGGAACCATGCAGAAACCTTGAAAGAGCAGAACACGGATCTTGCAACTATGTCTTCCCA
                                                    APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide and Methods
Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                                                                                                                  Version #1.30
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APPLICATION DATA:

APPLICATION NUMBER: 09/103,489

FILING DATE: 1998-06-24

ATTORNEY/AGENT INFORMATION:

RAME: Cohen, Charles E.

REGISTRATION NUMBER: 34,565

REFERENCE/DOCKET NUMBER: 38-21 (10700)A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 537-624

TELEFAX: (314) 537-6047

INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-681-972-2 (1-50) x US-09-829-381A-9 (1-500)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279 GCTCACAAATGTATTTGTTACTTCCCATGT 308
                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 AlaHisLysCysIleCysTyrPheProCys 50
                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATEN
COMPTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NO: 9:
Sequence 9, Application US/09829381A Patent No. US20020144306A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-681-972-9; Sequence 9, Application US/10681972; Publication No. US20040064850Al; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 500 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.17e-32
296.00
98.00%
96.00%
97.05%
                                                                                                                                                                                                                                                                                           ZIP: 63198
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Best Local Similarity:
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APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control TITLE OF INVENTION: Plant Pathogenic Fungi
FILE REPERENCE: 38-21 (10700) C.
CURRENT APPLICATION NUMBER: US/10/681, 972
CURRENT PILING DATE: 2003-10-09
PRIOR FILING DATE: 2001-04-09
PRIOR PILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SSOTHWARE: Patentin version 3:1
SSOTHWARE: Patentin version 3:1
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Mismatches:
Indels:
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       Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                   US-10-681-972-2 (1-50) x US-09-829-381A-12 (1-286)
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Matches:
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                                                                                                                                                                                                                                                                                                                  41 AlaHisLysCysIleCysTyrPheProCys 50
                                                                              Indels:
                                                                                                   Gaps:
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Publication No. US20040064850A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
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305.00
100.00%
100.00%
       1.37e-33
305.00
100.00%
100.00%
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Best Local Similarity:
                                         Percent Similarity:
Best Local Similarity:
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US-09-829-381A-9
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                                                                                Query Match:
           Pred. No.:
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APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Wannie C.
APPLICANT: Rosenberger, Cindy A.
TITLE OF INVENTION: Plant Pathogenic Fungi
FILE OF INVENTION: Plant Pathogenic Fungi
FILE OF INVENTION: Plant Pathogenic Fungi
FILE CHORENT APPLICATION NUMBER: US/10/681,972
CURRENT APPLICATION NUMBER: US/99/829,381D
PRIOR APPLICATION NUMBER: 09/103,489
PRIOR FILING DATE: 2001-04-09
FRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1998-06-24
ATTORNEY/AGBYT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET WINBER: 38-21 (10700)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 537-6224
TELEFAX: (314) 537-647
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: other nucleic acid

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "synthetic DNA"

US-09-829-381A-16
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Indels:
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FILING DATE: 09-Apr-2001
CLASSIFICATION: «CINKNOWN»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/103,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/10681972 Publication No. US20040064850A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Synthetic
US-10-681-972-16
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96.00%
90.00%
92.79%
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Best Local Similarity:
Query Match:
DB:
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    APPLICANT: Liang, Jihong
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: Shah, Dilip M.
APPLICANT: W. Younie S.
APPLICANT:
TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Contro
TITLE OF INVENTION: Plant Pathogenic Fungi
FILE REFERENCE: 38-21 (10700) C
CURRENT APPLICATION NUMBER: US/10/681,972
CURRENT FILING DATE: 2003-10-09
PRIOR FILING DATE: 2001-04-09
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Version 3.1
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 AAGTIGIGCGAGAGTCCAAGIGGAACAIGGICAGGCGIGIGIGGGAAIAAIAACGCAIGC
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Sequence 16, Application US/09829381A
Patent No. US20020144306A1
GENERAL INFORMATION:
APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
Rosenberger, Cindy A.
TITLE OF INVENTION: Attifungal Polypeptide and Methods for
Controlling Plant Pathogenic Fungi
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ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: US/09/829,381A
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98.00%
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                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Alyssum spp
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Best Local Similarity:
Query Match:
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21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
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Mismatches:
Indels:
                                               Conservative:
Mismatches:
Indels:
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APPLICANT: Fant, Franky
APPLICANT: Borremans, Frans
APPLICANT: Borremans, Frans
APPLICANT: Borremans, Genoveva
APPLICANT: Biltima, Lolke
APPLICANT: Milena, Lolke
APPLICANT: Wouter
APPLICANT: Broaper, Wilhelmus
APPLICANT: Broaper, Wilhelmus
APPLICANT: Brockeart, Wilhelmus
APPLICANT: Rees, Sarah
TITLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: 50094PDDIV (1002)
FILE REFERENCE: 50094PDDIV (1002)
FILE REFERENCE: 5003-03-13
FRIOR FILING DATE: 1998-08-07
PRIOR FILING DATE: 1998-08-07
PRIOR FILING DATE: 1996-12-12
PRIOR FILING DATE: 1996-12-12
PRIOR FILING DATE: 1996-12-12
PRIOR FILING DATE: 1996-12-12
PRIOR FILING DATE: 1996-12-12
PRIOR FILING DATE: 1996-12-12
PRIOR FILING DATE: 1996-12-12
PRIOR FILING DATE: 1995-12-13
NUMBER OF SEQ ID NOS: 141
SOCTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 45
LENGER DATE: 1414
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Matches:
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              Length:
Matches:
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283.00
96.00%
90.00%
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96.00%
90.00%
92.79%
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                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-10-388-361A-45
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Alignment Scores:
Pred. No.:
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ZIP: 20005
ZIP: 20005
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/759,584
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                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                          US-10-681-972-2 (1-50) x US-10-681-972-16 (1-285)
                                                                                                                                                                                                                                                                                                                                          241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BROEKGERT, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: OSBORN, RUBERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, UOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: CUSHMAN DARBY & CUSHMAN 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PADED APPLICATION DATA:
APPLICATION NUMBER: 08/377,687
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 48, Application US/09759584
Patent No. US20010014732A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 9904
TELECHHONE: 202-861-3000
TELEFRAX: 202-822-0944
                     1.66e-30
283.00
96.00%
90.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 414 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: WASHINGTON STATE: D.C.
                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , NAME/KEY:
; LOCATION:
US-09-759-584-48
       Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                               US-09-759-584-48
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CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE: Charles E. Cohen, Monsanto Company, BB4F
STREET: 700 Chesterfield Village Parkway No. US20020144306Alth
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 AAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ArgleuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reference Roberts Cindy A. RITLE OF INVENTION: Antifungal Polypeptide and Methods Controlling Plant Pathogenic Fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19950
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/732,561
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches:
Indels:
                                                                                                                                                                                                                                                    FILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/01672
FILING DATE: 20-UN-1997
ATTORNEY/AGENT INPORMATION:
NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
TELEPHONE: 33,712
TELEPHONE: (302) 886-1699
INFORMATION FOR SEQ. ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-681-972-2 (1-50) x US-09-732-561-13 (1-403)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 GCTCACAAATGTATCTGCTACTTCCCATGT 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17, Application US/09829381A Patent No. US20020144306A1 GENERAL INFORMATION:
                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/202,638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Liang, Jihong
Shah, Dilip M.
Wu, Yonnie S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.3e-29
278.00
96.00%
88.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 403 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 403 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-829-381A-17
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Pred. No.:
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    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
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166 AAGAATCAGIGCATTAACCTIGAGAAAGCACGACATGGATTCTIGCAACTATGTCTTCCCA 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ArgieuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys
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8 3 3 0 0 0 0 0 0 0
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APPLICANT: Thomma, ball
APPLICANT: Terras, Franky
APPLICANT: Penninckx, Iris
APPLICANT: Manners, John
APPLICANT: Manners, John
APPLICANT: Manners, John
TITLE OF INVENTION: Plant Protection Method
INWHER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZENECA AG Products
STREET: 1800 Concord Pike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                           Sequence 19, Application US/10006252A

Publication No. US20020152498A1

GENERAL INFORMATION:
APPLICANT: De Samblanx, Genoveva
APPLICANT: De Samblanx, Genoveva
APPLICANT: Broekaert, Willem
APPLICANT: Reses, Sarah
ITLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: SIN-034DV
CURRENT PILING DATE: 2001-12-04
CURRENT PILING DATE: 2001-12-04
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 09/077,951
PRIOR FILING DATE: 1995-12-13
PRIOR FILING DATE: 1995-12-13
PRIOR FILING DATE: 1995-12-13
PRIOR FILING DATE: 1996-12-12
NUMBER OF SEQ ID NOS: 77
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226 derekakarararenderakerreterrar 255
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                                                                    41 AlaHisLysCysIleCysTyrPheProCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13, Application US/09732561
Patent No. US20020035738A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.69e-30
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96.00%
90.00%
92.79%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA; CRGANISM: Raphanus sativus
US-10-006-252A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                       RESULT 11
US-10-006-252A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-732-561-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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21 ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro
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                                                                                                                                                                                               285
43
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/759,584
                                                                                                                                                                                                 Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99042/SEE.36525/US/A
                                                                                                                                                                                                                                                            Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                          US-10-681-972-2 (1-50) x US-10-681-972-17 (1-285)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 AlaHisLysCysIleCysTyrPheProCys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 50, Application US/09759584
Patent No. US20010014732A1
GENERAL INFORMATION:
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: CSBORN, RUPERT W.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: TENRAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATE:
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION WUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SI
TELECOMMUNICATION INFORMATION:
SOFTWARE: Patentin version 3.1
SEQ ID NO 17
LENGTH: 285
                                                             TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                               3.02e-29
274.00
94.00%
86.00%
89.84%
                                                                                                  FEATURE:
OTHER INFORMATION: Synthetic US-10-681-972-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20002
                                                                                                                                                                                   Alignment Scores:
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                                                                                                                                                                                                     Pred. No.:
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Sequence 17, Application US/10681972

Publication No. US20040064850A1

GENERAL INFORMATION:

APPLICANT: Liang, Jihong

APPLICANT: Shah, Dilip M.

APPLICANT: Rosenberger, Cindy A.

TITLE OF INVENTION: Antifungal Polypeptide ALYAFP from Alyssum and Methods for Control

TITLE OF INVENTION: Plant Pathogenic Fungi

FILE REFRENCE: 38-21 (10700) C.

CURRENT APPLICANTON NUMBER: US/10/601,972

CURRENT FILING DATE: 2003-10-09

PRIOR FILING DATE: 2001-04-09

PRIOR FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 20
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                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 4 E O O
                                                                                                                                                                                                                                       APPLICATION NUMBER: 09/103,489
FILING DATE: 1998-06-24
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21 (10700)A
TELEPHONE: (314) 537-624
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "synthetic DNA" SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-681-972-2 (1-50) x US-09-829-381A-17 (1-285)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 GCTCACAAGTGCATCTGCTACTTTCCATGC 270
                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/829,381A
FILING DATE: 09-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 AlaHisLysCysIleCysTyrPheProCys 50
                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.02e-29
274.00
94.00%
86.00%
89.84%
    COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
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Best Local Similarity:
Query Match:
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TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MILECULE TYPE: CDNA
FEATURE:
MANE/KEY: CDS
LOCATION: 43..282
US-09-759-584-58
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Alignment Scores:		,	į
Pred. No.:	3.06e-29	Length:	288
Score:	274.00	Matches:	43
Percent Similarity:	94.00%	Conservative:	4
Best Local Similarity:	86.00%	Mismatches:	e
\overline{a}	89.84%	Indels:	0
	65	Gaps:	0

US-10-681-972-2 (1-50) x US-09-759-584-58 (1-288)

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Search completed: May 18, 2004, 22:55:50 Job time: 290 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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(without alignments) 631.870 Million cell updates/sec US-10-681-972-2 305 1 RLCERPSGTWSGVCGNNNAC......EHGSCNYVFPAHKCICYFPC 50 May 18, 2004, 20:22:48 ; Search time 2363 Seconds OM protein - nucleic search, using frame_plus_p2n model Title: Perfect score: Run on:

27513289 segs, 14931090276 residues Total number of hits satisfying chosen parameters: 0.0 0.0 0.0 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext **BLOSUM62** Scoring table: Searched:

Sequence:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Command line parameters:
-MODEL=frame+ p2n.model -DEV=x1h
-MODEL=frame+ p2n.model -DEV=x1h
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-Q=/cgn2_1/USPTO_spool/US106B1972/runat_17052004_151740_4363/app_query.fasta_1.199
-DB=EST -Q=VT=fastap -SUFFIX=p2n.ret -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNINS=bits -START=1 -END=1 - MARRIX=blosum62 -TRANS=buman40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-USER=VS106B1972_@CGN 1 1_2135_@runat_17052004_151740_4363 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NGS_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DBV_TIMEOUT=120 -WARN TIMEOUT=30 -THEADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

EST: *

Database :

em_gss_rod:*
em_gss_pbg:*
em_gss_vrl:*
gb_gssl:* em_esthum:
em_estin:
em_estin:
em_estov:
em_estop:
em_estro:
em_btc:
gb_est::
gb_est2:*
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gb_est2:*
gb_est3:*
em_estfun:* em_gss_hum:* em_gss_inv:* vrt:* fun:* em gss pln:* em gss mam:* em_gas_mus:* em_gas_pro:* em_estom: * em estba:* em gss

gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

EST 10-JUL-2003 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica. CD833779 408 bp mRNA linear EST 10-JUL-2003 BN45.001115F010914 BN45 Brassica napus CDNA clone BN45001115, mRNA CD833779.1 GI:32515719 EST. Brassica napus (rape) Brassica napus sequence. DEFINITION ORGANISM RESULT 1 CD833779 ACCESSION VERSION KEYWORDS SOURCE

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                                                                                  93. The Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
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Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
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Genoplante, a major partnership french program in plant genomics
Uppublished (2003)
Contact: Genoplante
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                                                            Contact: Genoplante
Genoplante
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CD832625 BN40.064A14F011227 BN40 Brassica napus cDNA clone BN40064A14, mRNA sequence.
CD832625.1 GI:32514565
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Contact: Genoplante
Genoplante
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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CD826491 421 bp mRNA linear EST 10-JUL-2003
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sequence.
                                       CD833944 110-JUL-2003 RRNA linear EST 10-JUL-2003 BN45.040B07F011019 BN45 Brassica napus cDNA clone BN45040B07, MRNA
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Brassica napus
Brassica napus
Brassica napus
Brassica napus
Brassica napus
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
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Tel: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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                                                                                                                                                           203 AAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGGATCTTGCAACTATGTCTTCCCA 262
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
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Genoplante, a major partnership french program in plant genomics
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Contact: Genoplante
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                 US-10-681-972-2 (1-50) x CD832625 (1-418)
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II, Brassicales, Brassicaceae, Brassica.
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Genoplante, a major partnership french program in plant genomics (Unpublished (2003)
Contact: Genoplante
Genoplante
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Tel: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
                                                             93, The Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
Fhis sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
Genoplante, a major partnership french program in plant genomics Unpublished (2003)
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Matches:
Conservative:
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CD831111.1 GI:32513051
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283.00
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                                   Contact: Genoplante
Genoplante
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CD833977 421 bp mRNA linear EST 10-JUL-2003 BN45.040D05F011019 BN45 Brassica napus cDNA clone BN45040D05, mRNA sequence.
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Brassica napus
Brassica napus
Brassica napus
Brassica napus
Brassica napus
Brassica napus
Brassica napus
Spermatophyta; Virialplantae; Streptophyta; Embryophyta; Tracheophyta;
rosids; eurosids II;
Brassicales; Brassicaceae; Brassica.

Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante.info.infobiogen.fr).
Location/Qualifiers
                                                                                                                                                                                                                                                                           1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

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CD831294 110-JUL-2003
BN40.058N13F011019 BN40 Brassica napus cDNA clone BN40058N13, mRNA
CD827413 426 bp mRNA linear EST 10-JUL-2003
BN25.067G02F020123 BN25 Brassica napus cDNA clone BN25067G02, mRNA
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                                                                                                                                                         Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Byermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
(Dases I to 426)
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                                                                                                                                                                                                                                                                                                                                       93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
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Genoplante, a major partnership french program in plant genomics
Unpublished (2003)
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Unpublished (2003)
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CD827413.1 GI:32509353
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Mukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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Contact: Genoplante
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RESULT 10 CD827413

No.:

Score:

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CD834068 446 bp mRNA linear EST 10-JUL-2003 BN45.040H17F011019 BN45 Brassica napus cDNA clone BN45040H17, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                              1 ArgLeuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAsnAlaCys 20
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Contact: Genoplante
Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
Fins sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com
                                                                                                                                                                                                                                       1 ArgleuCysGluArgProSerGlyThrTrpSerGlyValCysGlyAsnAsnAlaCys
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Matches:
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Brassica napus (rape)
Brassica napus
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CD834068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201 AAGAATCAGTGCATTAACCTTGAGAAAGCACGACATGGATCTTGCAACTATGTCTTCCCA 260
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Contact: Genoplante
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                73. rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (http://www.genoplante.com
and http://genoplante-info.infobiogen.fr).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 AlahisiysCysileCysTyrPheProCys 50
                                                                                                                                                                         /organism="Brassica napus"
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CD831479.1 GI:32513419
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92.79%
   Contact: Genoplante
Genoplante
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Query Match:
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                                                                                                                                                                                 CDB32592 447 bp mRNA linear EST 10-JUL-2003
BN40.063015F011228 BN40 Brassica napus cDNA clone BN40063015, mRNA
sequence.
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Wharryora, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
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                                                           156 AAGTTGTGCGAGAGGCCAAGTGGGACATGGTCAGGAGTCTGTGGAAACAATAACGCATGC 215
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                                         ArgAsnGlnCysArgAsnLeuGluArgAlaGluHisGlySerCysAsnTyrValPhePro 40
                                                                                                                                                                                                                                                                                                                                                                                                                                               93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 10
Fax: 33 1 69 47 54 10
Fhis sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Brassica napus"
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/cultivar="Jet neuf"
                                                                                                        41 AlaHisLysCysIleCysTyrPheProCys 50
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CD832592.1 GI:32514532
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283.00
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Genoplante
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Brassica napus Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica. 1 (bases 1 to 450)
                                                                                                                                                                    Genoplante. Genoplante, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplante
Genoplante
                                                                                                                                                                                                                                                                                                                                     This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 AAGTIGIGCGAGAGGCCAAGIGGACAIGGICAGGAGICIGIGGAACAAIAACGCAIGI
                                                                                                                                                                                                                                                                   93, The Henri Rochefort 91025 EVRY CEDEX France Tel: 33 1 69 47 54 00 Fax: 33 1 69 47 54 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                      1. .450
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CD834611.1 GI:32516551
                                           Brassica napus (rape)
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